

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:11:12 ; Search time 36 Seconds  
(without alignments)  
658.850 Million cell updates/sec

Title: US-09-965-528-16

Perfect score: 964

Sequence: 1 MAARCLCLSLLLSTCVALL.....FSEWGSFHAAPVRELSPLDL 178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /SID82/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID82/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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21: /SID82/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID82/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	964	100.0	178	22 AAB48072	Human extracellular
2	378.5	39.3	95	20 AAY05276	Pancreatic polypep
3	186	19.3	36	19 AAW76722	Pancreatic polypep
4	186	19.3	36	21 AAB12179	Human pancreatic p
5	186	19.3	36	21 AAY87962	Human neuropeptide
6	186	19.3	36	21 AAY53658	Amino acid sequenc
7	186	19.3	36	22 AAB91217	Pancreatic polypep
8	186	19.3	36	22 AAU06196	Mammalian pancreat
9	177	18.4	36	21 AAY53657	Amino acid sequenc
10	139	14.4	36	21 AAB12180	Rat pancreatic pol

11	139	14.4	36	21 AAY87963	Rat neuropeptide P
12	139	14.4	36	22 AAB91221	Pancreatic polypep
13	114	11.8	36	22 AAB91220	Pancreatic polypep
14	110	11.4	36	11 AAR07276	Porcine small inte
15	110	11.4	36	22 AAB91226	Peptide YY SEQ ID
16	109	11.3	97	21 AAB08020	Amino acid sequenc
17	109	11.3	176	22 AAG75364	Human colon cancer
18	107	11.1	20	21 AAY53660	Amino acid sequenc
19	107	11.1	36	22 AAB91109	Parathyroid hormon
20	104	10.8	223	22 AAO06156	Human polypeptide
21	103.5	10.7	97	20 AAY43334	Neuropeptide Y. S
22	103.5	10.7	97	20 AAY23828	Human prepro-neuro
23	103.5	10.7	97	21 AAB35660	Human neuropeptide
24	103.5	10.7	97	21 AAY57078	Human neuropeptide
25	103.5	10.7	97	22 AAE07919	Human neuropeptide
26	103.5	10.7	97	22 AAE07955	Human neuropeptide
27	103.5	10.7	97	22 AAB85107	Human neuropeptide
28	103.5	10.7	97	22 AAB85118	Human neuropeptide
29	103.5	10.7	97	22 AAB80278	Human prostate can
30	103.5	10.7	97	23 AAO18305	Human neuropeptide
31	103.5	10.7	97	23 AAY92665	Human neuropeptide
32	102	10.6	216	21 AAO18054	MUC-1 analogue con
33	102	10.6	3014	22 AAU68533	Human novel cytoki
34	102	10.6	3014	22 AAU02196	Seven-pass transme
35	102	10.6	3028	22 AAE08586	Human NOV7 protein
36	100.5	10.4	505	18 AAW23275	Bordetella pertuss
37	99	10.3	532	22 ABG20464	Novel human diagno
38	99	10.3	36	11 AAR07277	Porcine small inte
39	99	10.3	36	15 AAR62050	Human peptide YY (
40	99	10.3	36	15 AAR62049	Porcine peptide YY
41	99	10.3	36	17 AAR97741	Porcine peptide YY
42	99	10.3	36	17 AAR97741	Porcine peptide YY
43	99	10.3	36	18 AAW15365	Human peptide YY
44	99	10.3	36	19 AAW51800	[im-DMP-His26]-PY
45	99	10.3	36	19 AAW51801	Porcine peptide YY

#### ALIGNMENTS

#### RESULT 1

AA848072  
ID AAB48072 standard; protein; 178 AA.

XX  
AC AAB48072;

XX  
AC AAB48072;

XX  
AC AAB48072;

XX  
AC AAB48072;

XX  
AC AAB48072;

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AC AAB48072;

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AC AAB48072;

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AC AAB48072;

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AC AAB48072;

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AC AAB48072;

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AC AAB48072;

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AC AAB48072;

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AC AAB48072;

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AC AAB48072;

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AC AAB48072;

XX  
AC AAB48072;

PI Azimzai Y, Lu DAM, Patterson C;  
XX WPI; 2001-025021/03.  
DR N-PSDB; AAC8#308.  
XX  
PT New human extracellular signaling nucleic acids and polypeptides useful  
PT for diagnosing, treating and preventing infections and  
PT gastrointestinal, neurological, reproductive, and  
PT autoimmune/inflammatory disorders -  
XX  
XX Claim 1; Page 93; 114pp; English.  
XX  
CC The invention provides human extracellular signaling molecules (EXCS)  
CC and polynucleotides which identify and encode EXCS. EXCS can be  
CC expressed by standard recombinant methodology. The amino acid and nucleic  
CC acid sequences of EXCS are useful for diagnosing, treating and  
CC preventing infections and gastrointestinal (peptic ulcer, dysphagia,  
CC pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular  
CC disease, stroke), reproductive (infertility, ovulatory defects,  
CC endometriosis), autoimmune/inflammatory (actinic keratosis, acquired  
CC immunodeficiency syndrome (AIDS), Addison's disease), and cell  
CC proliferative disorders including cancers (of the breast, adrenal gland,  
CC bone). They may also be used to treat fatal familial insomnia,  
CC nutritional and metabolic diseases of the nervous system, myopathies,  
CC mental disorders (anxiety, schizophrenia, mood), as well as infections  
CC caused by parasites (malaria, leishmania, trypanosoma), viral  
CC (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,  
CC staphylococcus, bacillus), and fungal (aspergillus, blastomycetes,  
CC dermatophytes) agents. The nucleic acids, polypeptides, antagonists,  
CC agonists, pharmaceutical compositions, and antibodies may also be used  
CC for treating or preventing disorders associated with increased or  
CC decreased expression or activity of EXCS. EXCS polynucleotides may also  
CC be used to detect and quantify gene expression in biopsied tissues in  
CC which expression of EXCS may be correlated with the disease, to determine  
CC presence or excess expression of EXCS, to monitor regulation of EXCS  
CC levels during therapeutic intervention, to detect the presence of  
CC associated disorders, as targets in microarray, to generate hybridization  
CC probes, and to detect differences in gene sequences among normal, carrier  
CC or affected individuals. Antibodies may also be used in diagnosing  
CC disorders, in monitoring patients being treated with EXCS agonists,  
CC antagonists or inhibitors. Sequences AAB48057-B48082 represent the EXCS  
CC of the invention.  
XX  
SQ Sequence 178 AA;  
  
Query Match 100.0%; Score 964; DB 22; Length 178;  
Best Local Similarity 100.0%; Pred. No. 3e-83;  
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 MAARCLSLLLSTCVALLQPLGAGAPLEPVVPGDNATPEQMAQYAADLRRYINML 60  
1 MAARCLSLLLSTCVALLQPLGAGAPLEPVVPGDNATPEQMAQYAADLRRYINML 60  
  
61 TRPRCVQLGREIPAGTGLPLHIGHTLSPAPAPSPALGKTKTGLHLCSTGLDQCALGK 120  
61 TRPRCVQLGREIPAGTGLPLHIGHTLSPAPAPSPALGKTKTGLHLCSTGLDQCALGK 120  
  
121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSHPAAVPRELSPLDL 178  
121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSHPAAVPRELSPLDL 178

KW therapy; food intake-related disorder; obesity; anorexia; bulimia;  
KW Parkinson's disease; acute heart failure; hypotension; hypertension;  
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;  
KW asthma; allergy; benign prostatic hypertrophy; psychotic disorder;  
KW neurological disorder; cancer.  
XX  
OS Homo sapiens.  
XX  
PN EP908515-A2.  
XX  
PD 14-APR-1999.  
XX  
XX 15-JUN-1998; 98EP-0304691.  
XX  
PR 16-SEP-1997; 97EP-0307187.  
XX  
PA (SMIK ) SMITHLINE BEECHAM PLC.  
XX  
PI Southan CD;  
XX  
XX WPI; 1999-217067/19.  
XX  
XX N-PSDB; AAX28413.  
XX  
XX New pancreatic neurotrophic polypeptide and polynucleotide, useful  
XX as diagnostic reagents and for prevention and treatment of cancer,  
XX asthma and schizophrenia  
XX  
XX Claim 10; Page 14-15; 16pp; English.  
XX  
CC This sequence is the pancreatic polypeptide of the invention. The  
CC pancreatic polypeptide is a member of the neurotrophic family. Pancreatic  
CC polynucleotides and polypeptides are useful for diagnosing susceptibility  
CC to diseases by detecting mutations in the pancreatic gene, and can  
CC diagnose diseases associated with pancreatic polypeptide imbalance by  
CC determining pancreatic polypeptide levels. Pancreatic polypeptides can be  
CC used to screen for agonists and antagonists which bind the polypeptide by  
CC observing the binding, stimulation or inhibition of pancreatic  
CC polypeptide activity. These can be used in treatment to activate or  
CC inhibit pancreatic polypeptide activity, in addition to direct  
CC administration of antisense sequences and soluble pancreatic polypeptides  
CC to prevent expression, or pancreatic polynucleotides to treat conditions  
CC associated with a lack of pancreatic polypeptide. Gene therapy may also  
CC be used to affect endogenous pancreatic polypeptide production, and  
CC pancreatic polypeptide epitopes are used as vaccines to generate an  
CC immunological response. Anti-pancreatic polypeptide antibodies are useful  
CC for inducing an immune response to immunize and prevent disease, and for  
CC isolating pancreatic clones or purifying the polypeptide by affinity  
CC chromatography. Diseases diagnosed, prevented or treated include: food  
CC intake-related disorders e.g. obesity, anorexia and bulimia; Parkinson's  
CC disease; acute heart failure; hypotension; hypertension; urinary  
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;  
CC asthma; allergies; benign prostatic hypertrophy; and psychotic and  
CC neurological disorders including anxiety, schizophrenia, manic  
CC depression, delirium, dementia, severe mental retardation and  
CC dyskinesias; and cancer and pain.  
XX  
SQ Sequence 95 AA;  
  
Query Match 39.3%; Score 378.5; DB 20; Length 95;  
Best Local Similarity 47.2%; Pred. No. 3e-28;  
Matches 84; Conservative 4; Mismatches 7; Indels 83; Gaps 1;  
  
1 MAARCLSLLLSTCVALLQPLGAGAPLEPVVPGDNATPEQMAQYAADLRRYINML 60  
1 MAARCLSLLLSTCVALLQPLGAGAPLEPVVPGDNATPEQMAQYAADLRRYINML 60  
  
61 TRPRCVQLGREIPAGTGLPLHIGHTLSPAPAPSPALGKTKTGLHLCSTGLDQCALGK 120  
61 TRPRCVQLGREIPAGTGLPLHIGHTLSPAPAPSPALGKTKTGLHLCSTGLDQCALGK 120  
  
121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSHPAAVPRELSPLDL 178  
121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSHPAAVPRELSPLDL 178  
63 -----HRYGKRKEDTLAFSEWGSHPAAVPRELSPLDL 95

## RESULT 3

AAW76722  
ID AAW76722 standard; peptide; 36 AA.

AC AAW76722;  
XX

DT 13-JAN-1999 (first entry)

XX Pancreatic polypeptide fragment for NIDDM treatment.

XX Non-insulin dependent diabetes mellitus; NIDDM; hepatic glucose;  
KW pancreatic polypeptide; PP; treatment; Gs protein alpha subunit;  
KW inhibitor; cyclic adenosine monophosphate; cAMP; glucagon; secretion;  
KW exocrine pancreas; beta cell; pancreatic islet hypertrophy; insulin;  
KW neurotrophin Y; hyperglycaemia.

XX Homo sapiens.

OS US5830434-A.

XX 03-NOV-1998.

PF 26-FEB-1997; 97US-0806203.

XX 26-FEB-1997; 97US-0806203.

PR (UYSC-) UNIV SOUTH CAROLINA MEDICAL RES FOUND.

PA Gettys T, Taylor IL;

PI WPI; 1998-609185/51.

DR Treatment of non-insulin-dependent diabetes mellitus - with

PT pancreatic polypeptide or C-terminal fragment

XX Disclosure; Column 3; 11pp; English.

XX This human pancreatic polypeptide fragment is used in a method for  
CC treating non-insulin-dependent diabetes mellitus (NIDDM). The method  
CC involves administering a composition comprising pancreatic polypeptide or  
CC C-terminal pancreatic polypeptide fragment in a carrier. Screening a  
CC composition for the ability to treat NIDDM is also possible and involves  
CC determining if the composition decreases hepatic expression of the  
CC alpha subunit of a Gs protein in a liver cell plasma membrane, thereby  
CC inhibiting stimulation of cyclic adenosine monophosphate (cAMP) by  
CC glucagon, determined if the composition binds the vagal nuclear complex  
CC and inhibits secretions of digestive enzymes by the exocrine pancreas,  
CC thereby inhibiting beta cell and pancreatic islet hypertrophy or  
CC determining if the composition binds the arcuate nucleus in the  
CC hypothalamus and potentiates the effect of leptin in reducing  
CC neurotrophin Y synthesis, thereby enhancing insulin sensitivity and  
CC reversing the effects of neurotrophin Y. The NIDDM treatment method  
CC decreases hyperglycaemia and increases insulin sensitivity without  
CC additional detrimental effects.

XX Sequence 36 AA;

Query Match 19.3%; Score 186; DB 19; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVYPCGNATPQMAQYAADLRRYINMLTRPR 64

Db 1 APLEPVYPCGNATPQMAQYAADLRRYINMLTRPR 35

## RESULT 4

AA12179  
ID AAB12179 standard; peptide; 36 AA.

XX AAB12179;

AC

XX 20-JUN-2001 (first entry)

DT Human pancreatic polypeptide.

XX Human; neurotrophin Y; luteinizing hormone; reproductive system;  
KW NPY; NPY-Y4 receptor; precocious puberty; pancreatic polypeptide;  
KW polycystic ovary syndrome; endometriosis; benign prostatic hyperplasia;  
KW delayed puberty; amenorrhea; breast cancer; prostate cancer; PP.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT Modified-site 36

FT /note= "C-terminal amide"

XX WO200030674-A1.

XX 02-JUN-2000.

XX 26-NOV-1999; 99WO-GB03963.

XX 26-NOV-1998; 98GB-0025969.

PR 13-MAY-1999; 99GB-0011178.

XX (FERR ) FERRING BV.

PA Broqua P, Akinsanya K, Hayward A;

PI WPI; 2000-399931/34.

XX Treating human reproductive disorders such as amenorrhea, delayed  
PT puberty, polycystic ovary syndrome and endometriosis, comprises  
PT administering a neurotrophin Y-Y4 receptor ligand -

XX Disclosure; Page 2; 17pp; English.

XX Neurotrophin Y (NPY) (AAB12177) has a number of effects on the  
CC reproductive system. NPY is one of a family of neuropeptides. Other  
CC members of the family include peptide YY (PYY, see AAB12177), and the  
CC present sequence, human pancreatic polypeptide (HPP). Rat pancreatic  
CC polypeptide is described in AAB12180. Selective NPY-Y4 receptor agonists  
CC have been found (see AAB12181 to AAB12183). The NPY-Y4 receptor agonists  
CC cause an increase in the circulating levels of luteinizing hormone (LH),  
CC and hence improve the fertility of animals with compromised reproductive  
CC function. The NPY-Y4 agonists may be used to treat human reproductive  
CC disorders such as delayed puberty and amenorrhea. In addition, NPY-Y4  
CC antagonists may be used to treat human reproductive disorders such as  
CC precocious puberty, endometriosis, polycystic ovary syndrome, benign  
CC prostatic hyperplasia and hormone-dependent neoplasias e.g. breast cancer  
CC and prostate cancer. The present sequence was used in a sequence homology  
CC comparison.

XX Sequence 36 AA;

Query Match 19.3%; Score 186; DB 21; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVYPCGNATPQMAQYAADLRRYINMLTRPR 64

Db 1 APLEPVYPCGNATPQMAQYAADLRRYINMLTRPR 35

RESULT 5

AA12179

ID AAY87962 standard; peptide; 36 AA.

XX AAY87962;

XX 18-SEP-2000 (first entry)

XX Human neurotrophin PP fragment.

XX Neuropeptide; human; treatment; reproductive disorder; neuropeptide Y;  
 KW endocrine; gynecological; cytostatic; puberty; endometriosis;  
 KW polycystic ovary syndrome; prostatic hyperplasia; amenorrhea.  
 XX Homo sapiens.  
 XX GB2344050-A.  
 XX 31-MAY-2000.  
 XX 26-NOV-1998; 98GB-0025969.  
 XX 26-NOV-1998; 98GB-0025969.  
 XX (FERR ) FERRING BV.  
 XX Akineanya K, Hayward A, Broqua P;  
 XX WPI; 2000-331548/29.  
 XX Compositions containing a neuropeptide Y Y4 receptor ligand selective  
 for the hypothalamic-pituitary-gonadal axis, for treatment of  
 PT reproductive disorders e.g. delayed or precocious puberty,  
 PT endometriosis and benign prostatic hyperplasia -  
 XX Disclosure; Page 2; 12pp; English.  
 XX This invention describes the novel use of a composition containing a  
 CC neuropeptide Y (NPY) Y4 receptor ligand for treatment of human  
 CC reproductive disorders. The products described in the invention have  
 CC endocrine, gynecological and cytostatic activity and can be used for the  
 CC treatment of reduced reproductive function, delayed puberty, supranormal  
 CC function of the reproductive organs, precocious puberty, endometriosis,  
 CC polycystic ovary syndrome, benign prostatic hyperplasia, impaired  
 CC reproductive function or amenorrhea. This sequence represents the human  
 CC PP neuropeptide which is used in the method of the invention.  
 XX  
 XX Sequence 36 AA;  
 XX  
 XX Query Match 19.3%; Score 186; DB 21; Length 36;  
 XX Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
 XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 30 APLEPVYVGDNATPEQMAQYAADLRRYINMLTRPR 64  
 DB 1 APLEPVYVGDNATPEQMAQYAADLRRYINMLTRPR 35  
 XX  
 XX RESULT 6  
 XX AAY53658  
 XX ID AAY53658 standard; protein; 36 AA.  
 XX AC AAY53658;  
 XX 22-FEB-2000 (first entry)  
 XX Amino acid sequence of the human pancreatic polypeptide.  
 XX Human; pancreatic polypeptide; transplanted pancreatic tissue viability;  
 KW graft damage; graft deterioration; immunosuppressive treatment; insulin;  
 KW pancreatic tissue; diabetic; clinical monitor;  
 KW early transplant viability; transplant survival.  
 XX Homo sapiens.  
 XX WO958979-A1.  
 XX 18-NOV-1999.  
 XX 13-MAY-1999; 99WO-AU00361.  
 XX 13-MAY-1998; 98AU-0003490.

XX (SES-) SOUTHEASTERN SYDNEY AREA HEALTH SERVICE.  
 PA (UNIX ) UNISEARCH LTD.  
 XX Tuck BE, Amaratunga AP, Brown AS, Bucknall MP, Duncan MW;  
 XX WPI; 2000-053124/04.  
 XX New method for monitoring transplanted pancreatic tissue viability in  
 PT mammal -  
 XX Disclosure; Fig 7; 70pp; English.  
 XX The present sequence represents a human pancreatic polypeptide. The  
 CC polypeptide is used in the method of the invention, for monitoring  
 CC transplanted pancreatic tissue viability. The method comprises screening  
 CC for the modulation of the level of a transplanted tissue derived molecule  
 CC or its derivative, e.g. pancreatic polypeptide, in the body fluid. The  
 CC method is useful for monitoring the viability of transplanted pancreatic  
 CC tissue in a mammal by screening for an increase or decrease in the level  
 CC of a transplanted tissue derived molecule. The method is an indicator of  
 CC graft damage or deterioration which would permit the commencement of  
 CC immunosuppressive treatment. The method is especially useful for  
 CC monitoring the viability of insulin producing foetal pancreatic tissue  
 CC which has been transplanted into diabetic patients. The method is also  
 CC useful as a non-invasive clinical monitor of early transplant viability  
 CC and on-going transplant survival.  
 XX  
 XX Sequence 36 AA;  
 XX  
 XX Query Match 19.3%; Score 186; DB 21; Length 36;  
 XX Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
 XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 30 APLEPVYVGDNATPEQMAQYAADLRRYINMLTRPR 64  
 DB 1 APLEPVYVGDNATPEQMAQYAADLRRYINMLTRPR 35  
 XX  
 XX RESULT 7  
 XX AAB91217  
 XX ID AAB91217 standard; Peptide; 36 AA.  
 XX AC AAB91217;  
 XX 22-JUN-2001 (first entry)  
 XX Pancreatic polypeptides (PP) peptide SEQ ID NO:391.  
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX Homo sapiens.  
 XX Synthetic.  
 XX WO200069900-A2.  
 XX 23-NOV-2000.  
 XX 17-MAY-2000; 2000WO-US33576.  
 XX 17-MAY-1999; 99US-0134406.  
 XX 10-SEP-1999; 99US-0153406.  
 XX 15-OCT-1999; 99US-0159783.  
 XX (CONJ-) CONJUCHEM INC.  
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
 XX WPI; 2001-112059/12.  
 XX Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity  
PS Disclosure; Page 325; 733pp; English.  
XX  
XX The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimide and maleimide groups) attached to  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity  
CC in vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention.  
XX  
XX Sequence 36 AA;  
SQ  
Query Match 19.3%; Score 186; DB 22; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 30 APLEPVPGDNATPEQMAQYAADLRRYINMLTRPR 64  
DB 1 APLEPVPGDNATPEQMAQYAADLRRYINMLTRPR 35  
RESULT 8  
AAU06196  
ID AAU06196 standard; peptide; 36 AA.  
XX  
AC AAU06196;  
XX  
DT 04-DEC-2001 (first entry)  
XX  
DE Mammalian pancreatic polypeptide (PP).  
XX  
KW Mammalian; brain aluminium concentration; central nervous system;  
KW CNS; peptide tyrosine-tyrosine receptor; PYY receptor; PP receptor;  
KW pancreatic polypeptide receptor; Alzheimer's disease; neurotropic;  
KW neuro protective.  
OS Mammalia.  
XX  
XX WO200158409-A2.  
PN  
XX 16-AUG-2001.  
PD  
XX  
XX 07-FEB-2001; 2001WO-US03952.  
PF  
XX  
XX 08-FEB-2000; 2000US-0499980.  
PR  
XX  
XX (UYNV-) UNIV NORTH CAROLINA STATE.  
PA  
XX  
XX Croom WJ, Berg BM, Taylor IL;  
PI  
XX  
XX WPI; 2001-550001/61.  
DR  
XX  
XX Reducing aluminium levels in the central nervous system, for the  
PT treatment of Alzheimer's disease comprises administration of a peptide  
PT tyrosine receptor agonist or a pancreatic polypeptide receptor agonist  
PT  
XX  
XX Disclosure; Page 6; 52pp; English.  
PS  
XX  
XX The present invention relates to a method of reducing aluminium levels

CC in the central nervous system (CNS). The method comprises administration  
CC of a peptide tyrosine-tyrosine (PYY) receptor agonist or a pancreatic  
CC polypeptide (PP) receptor agonist. The method is useful for the  
CC treatment of Alzheimer's disease and for reducing aluminium levels in  
CC the central nervous system, especially the brain, of a subject. The  
CC treatments are effective and do not impart excessive toxicological  
CC effects. The present sequence represents mammalian pancreatic PP.  
XX  
XX Sequence 36 AA;  
SQ  
Query Match 19.3%; Score 186; DB 22; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 30 APLEPVPGDNATPEQMAQYAADLRRYINMLTRPR 64  
DB 1 APLEPVPGDNATPEQMAQYAADLRRYINMLTRPR 35  
RESULT 9  
AAY53657  
ID AAY53657 standard; protein; 36 AA.  
XX  
XX AC AAY53657;  
XX  
XX 22-FEB-2000 (first entry)  
DT  
XX  
DE Amino acid sequence of the porcine pancreatic polypeptide.  
XX  
KW Pig; pancreatic polypeptide; transplanted pancreatic tissue viability;  
KW graft damage; graft deterioration; immunosuppressive treatment; insulin;  
KW pancreatic tissue; diabetic; clinical monitor;  
KW early transplant viability; transplant survival.  
XX  
OS Sus sp.  
XX  
XX WO9958979-A1.  
PN  
XX 18-NOV-1999.  
PD  
XX  
XX 13-MAY-1999; 99WO-AU00361.  
PF  
XX  
XX 13-MAY-1998; 98AU-0003490.  
PR  
XX  
XX (SESY-) SOUTHEASTERN SYDNEY AREA HEALTH SERVICE.  
PA (UNIX) UNISEARCH LTD.  
XX  
XX Tuch BE, Amaratunga AP, Brown AS, Bucknall MP, Duncan MW;  
PI  
XX  
XX WPI; 2000-053124/04.  
DR  
XX  
XX New method for monitoring transplanted pancreatic tissue viability in  
PT mammal  
XX  
XX Disclosure; Fig 7; 70pp; English.  
PS  
XX  
XX The present sequence represents a porcine pancreatic polypeptide. The  
CC polypeptide is used in the method of the invention, for monitoring  
CC transplanted pancreatic tissue viability. The method comprises screening  
CC for the modulation of the level of a transplant tissue derived molecule  
CC or its derivative, e.g. pancreatic polypeptide, in the body fluid. The  
CC method is useful for monitoring the viability of transplanted pancreatic  
CC tissue in a mammal by screening for an increase or decrease in the level  
CC of a transplant tissue derived molecule. The method is an indicator of  
CC graft damage or deterioration which would permit the commencement of  
CC immunosuppressive treatment. The method is especially useful for  
CC monitoring the viability of insulin producing foetal pancreatic tissue  
CC which has been transplanted into diabetic patients. The method is also  
CC useful as a non-invasive clinical monitor of early transplant viability  
CC and on-going transplant survival.  
XX  
XX Sequence 36 AA;  
SQ

Query Match 18.4%; Score 177; DB 21; Length 36;  
 Best Local Similarity 94.3%; Pred. No. 1.1e-09;  
 Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVPGDNATPEQMAQYAADLRRYINMLTRPR 64  
 DB 1 APLEVPGDDATPEQMAQYAAALRRYINMLTRPR 35

RESULT 10  
 AAB12180  
 ID AAB12180 standard; peptide; 36 AA.

XX AC AAB12180;  
 XX DT 20-JUN-2001 (first entry)  
 XX DE Rat pancreatic polypeptide.

KW Rat; neuropeptide Y; luteinizing hormone; reproductive system;  
 NPY; NPY-Y4 receptor; precocious puberty; pancreatic polypeptide;  
 polycystic ovary syndrome; endometriosis; benign prostatic hyperplasia;  
 delayed puberty; amenorrhea; breast cancer; prostate cancer; PP.

XX OS Rattus sp.

XX FH Key Location/Qualifiers  
 XX FT Modified-site 36  
 XX FT /note= "C-terminal amide"

XX PN W0200030674-A1.

XX PD 02-JUN-2000.

XX PF 26-NOV-1999; 99WO-GB03963.

XX PR 26-NOV-1998; 98GB-0025969.

XX PR 13-MAY-1999; 99GB-0011178.

XX PA (FERR ) FERRING BV.

XX PI Broqua P, Akinsanya K, Hayward A;

XX DR WPI; 2000-399931/34.

XX CC Treating human reproductive disorders such as amenorrhea, delayed  
 PT puberty, polycystic ovary syndrome and endometriosis, comprises  
 PT administering a neuropeptide Y-Y4 receptor ligand -

XX PS Disclosure; Page 2; 17pp; English.

XX CC Neuropeptide Y (NPY) (AAB12177) has a number of effects on the  
 CC reproductive system. NPY is one of a family of neuropeptides. Other  
 CC members of the family include peptide YY (PYY), see AAB12177), and the  
 CC present sequence, rat pancreatic polypeptide (RPP). Human pancreatic  
 CC polypeptide is described in AAB12179. Selective NPY-Y4 receptor agonists  
 CC have been found (see AAB12181 to AAB12183). The NPY-Y4 receptor agonists  
 CC cause an increase in the circulating levels of luteinizing hormone (LH)  
 CC and hence improve the fertility of animals with compromised reproductive  
 CC function. The NPY-Y4 agonists may be used to treat human reproductive  
 CC disorders such as delayed puberty and amenorrhea. In addition, NPY-Y4  
 CC antagonists may be used to treat human reproductive disorders such as  
 CC precocious puberty, endometriosis, polycystic ovary syndrome, benign  
 CC prostatic hyperplasia and hormone-dependent neoplasias e.g. breast cancer  
 CC and prostate cancer. The present sequence was used in a sequence homology  
 CC comparison.

XX SQ Sequence 36 AA;

Query Match 18.4%; Score 139; DB 21; Length 36;  
 Best Local Similarity 77.1%; Pred. No. 4.2e-06;  
 Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 30 APLEPVPGDNATPEQMAQYAADLRRYINMLTRPR 64  
 DB 1 APLEVPGDYATHEQRAQYETQLRRYINMLTRPR 35

RESULT 11  
 AAY87963  
 ID AAY87963 standard; peptide; 36 AA.

XX AC AAY87963;

XX DT 18-SEP-2000 (first entry)

XX DE Rat neuropeptide PP fragment.

XX KW Neuropeptide; rat; treatment; reproductive disorder; neuropeptide Y;  
 XX endocrine; gynecological; cytostatic; puberty; endometriosis;  
 XX polycystic ovary syndrome; prostatic hyperplasia; amenorrhea.

XX OS Rattus sp.

XX PN GB2344050-A.

XX PD 31-MAY-2000.

XX PF 26-NOV-1998; 98GB-0025969.

XX PR 26-NOV-1998; 98GB-0025969.

XX PA (FERR ) FERRING BV.

XX PI Akinsanya K, Hayward A, Broqua P;

XX DR WPI; 2000-331548/29.

XX CC Compositions containing a neuropeptide Y Y4 receptor ligand selective  
 PT for the hypothalamic-pituitary-gonadal axis, for treatment of  
 PT reproductive disorders e.g. delayed or precocious puberty,  
 PT endometriosis and benign prostatic hyperplasia -

XX PS Disclosure; Page 2; 12pp; English.

XX CC This invention describes the novel use of a composition containing a  
 CC neuropeptide Y (NPY) Y4 receptor ligand for treatment of human  
 CC reproductive disorders. The products described in the invention have  
 CC endocrine, gynecological and cytostatic activity and can be used for the  
 CC treatment of reduced reproductive function, delayed puberty, supranormal  
 CC function of the reproductive organs, precocious puberty, endometriosis,  
 CC polycystic ovary syndrome, benign prostatic hyperplasia, impaired  
 CC reproductive function or amenorrhea. This sequence represents the rat  
 CC PP neuropeptide which is used in the method of the invention.

XX SQ Sequence 36 AA;

Query Match 14.4%; Score 139; DB 21; Length 36;  
 Best Local Similarity 77.1%; Pred. No. 4.2e-06;  
 Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 30 APLEPVPGDNATPEQMAQYAADLRRYINMLTRPR 64  
 DB 1 APLEVPGDYATHEQRAQYETQLRRYINMLTRPR 35

RESULT 12  
 AAB91221  
 ID AAB91221 standard; Peptide; 36 AA.

XX AC AAB91221;

XX DT 22-JUN-2001 (first entry)

XX DE Pancreatic polypeptides (PP) peptide SEQ ID NO:395.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX Homo sapiens.  
 OS Synthetic.  
 OS WO200069900-A2.  
 XX 23-NOV-2000.  
 XX 17-MAY-2000; 2000WO-US13576.  
 XX 17-MAY-1999; 99US-0134406.  
 PR 10-SEP-1999; 99US-0153406.  
 PR 15-OCT-1999; 99US-0159783.  
 XX (CONJ-) CONJUCHEM INC.  
 PA Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 WPI; 2001-112059/12.  
 DR Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 PT Disclosure; Page 327; 733pp; English.  
 PS The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.  
 XX Sequence 36 AA;  
 SQ Query Match 14.4%; Score 139; DB 22; Length 36;  
 Best Local Similarity 77.1%; Pred. No. 4.2e-06;  
 Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
 QY 30 APLEPVPGDNATPEQMAQYAADLRRYINMLTRPR 64  
 DB 1 APLEPMYPGDYATHEQRAQYETQLRRYINMLTRPR 35  
 RESULT 13  
 ID AAB91220 standard; Peptide; 36 AA.  
 AC AAB91220;  
 XX 22-JUN-2001 (first entry)  
 DT Pancreatic polypeptides (PP) peptide SEQ ID NO:394.  
 DE Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX Homo sapiens.

OS Synthetic.  
 XX WO200069900-A2.  
 XX 23-NOV-2000.  
 XX 17-MAY-2000; 2000WO-US13576.  
 XX 17-MAY-1999; 99US-0134406.  
 PR 10-SEP-1999; 99US-0153406.  
 PR 15-OCT-1999; 99US-0159783.  
 XX (CONJ-) CONJUCHEM INC.  
 PA Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 WPI; 2001-112059/12.  
 DR Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 PT Disclosure; Page 326; 733pp; English.  
 PS The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.  
 XX Sequence 36 AA;  
 SQ Query Match 11.8%; Score 114; DB 22; Length 36;  
 Best Local Similarity 60.0%; Pred. No. 0.00096;  
 Matches 21; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
 QY 30 APLEPVPGDNATPEQMAQYAADLRRYINMLTRPR 64  
 DB 1 APSEPHHPGDQATQDQLAQYSDLYQYITFVTRPR 35  
 RESULT 14  
 ID AAR07276 standard; protein; 36 AA.  
 AC AAR07276;  
 XX 01-FEB-1991 (first entry)  
 DT Porcine small intestine YY peptide analogue #1.  
 DE porcine small intestine YY peptide; nerve-tropic activity.  
 KW Synthetic.  
 OS JP02225497-A.  
 XX 07-SEP-1990.  
 XX 27-FEB-1989; 89JP-0046089.  
 XX





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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:12:46 ; Search time 14 Seconds  
(without alignments)  
479.606 Million cell updates/sec

Title: US-09-965-528-16

Perfect score: 964  
Sequence: 1 MAAARLCISLLSLSTCVALL.....FSEWGSPHAAPRELSPDL 178

Scoring table: BLOSUM62

Gapop 10.0 , Gapekt 0.5

Searched: 174566 seqs, 37721826 residues

Total number of hits satisfying chosen parameters: 174566

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	964	100.0	178	9	US-09-965-528-16
2	378.5	39.3	95	10	US-08-757-712-2
3	186	19.3	36	12	US-10-016-969-1
4	103.5	10.7	97	9	US-10-002-048A-2
5	102	10.6	3014	10	US-09-737-149-2
6	99	10.3	36	12	US-10-016-969-2
7	99	10.3	36	12	US-10-038-045-4
8	96	10.0	36	12	US-10-038-045-2
9	94	9.8	36	12	US-10-038-045-1
10	93.5	9.7	508	9	US-10-057-136-20
11	93	9.6	410	9	US-10-078-650-14
12	92.5	9.6	1255	9	US-09-996-069-10
13	92	9.5	34	12	US-10-016-969-3
14	89	9.2	36	12	US-10-016-969-4
15	88	9.2	36	12	US-10-038-045-3
16	88	9.1	666	10	US-09-791-171-70
17	86	8.9	36	12	US-10-038-045-5
18	84.5	8.8	145	9	US-09-950-933A-45
19	84	8.7	34	12	US-10-016-969-5

20	84	8.7	1084	12	US-10-071-900-3	Sequence 3, Appli
21	83	8.6	1036	12	US-10-014-882-2	Sequence 2, Appli
22	81.5	8.5	365	10	US-09-876-187-4	Sequence 4, Appli
23	81.5	8.5	365	10	US-09-749-728B-15	Sequence 15, Appl
24	81	8.4	628	10	US-09-862-027-48	Sequence 48, Appl
25	81	8.4	726	10	US-09-770-689A-4	Sequence 4, Appli
26	81	8.4	803	10	US-09-770-689A-2	Sequence 2, Appli
27	81	8.4	5179	9	US-10-025-380-1068	Sequence 1068, Ap
28	81	8.4	5179	10	US-09-922-217-1068	Sequence 1068, Ap
29	81	8.4	5179	10	US-09-833-263-1068	Sequence 1068, Ap
30	80.5	8.4	100	9	US-09-965-131-6	Sequence 6, Appli
31	80	8.3	619	9	US-09-882-774-1	Sequence 1, Appli
32	79	8.2	207	10	US-09-343-954A-4	Sequence 4, Appli
33	79	8.2	207	10	US-09-912-436-4	Sequence 4, Appli
34	79	8.2	207	10	US-09-907-007-4	Sequence 4, Appli
35	78.5	8.1	163	9	US-09-854-133-41	Sequence 41, Appl
36	78.5	8.1	163	10	US-09-738-973-41	Sequence 41, Appl
37	78.5	8.1	755	10	US-09-919-497-57	Sequence 57, Appl
38	78.5	8.1	785	9	US-09-989-920-218	Sequence 218, App
39	78.5	8.1	891	9	US-09-976-059-18	Sequence 113, App
40	77.5	8.0	207	10	US-09-800-729-113	Sequence 113, App
41	77.5	8.0	208	10	US-09-800-729-151	Sequence 151, App
42	77.5	8.0	626	10	US-09-862-027-43	Sequence 43, Appl
43	77.5	8.0	635	9	US-09-738-626-6614	Sequence 6614, Ap
44	77.5	8.0	881	10	US-09-816-860A-2	Sequence 2, Appli
45	77	8.0	188	9	US-09-852-209A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1  
US-09-965-528-16  
; Sequence 16, Application US/09965528  
; Publication No. US20020187523A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: YUE, Henry  
; APPLICANT: LAL, Preeti  
; APPLICANT: BURFORD, Neil  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: LU, Dyung Aina M.  
; APPLICANT: PATTERSON, Chandra  
; TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES  
; FILE REFERENCE: PF-0701 USA  
; CURRENT APPLICATION NUMBER: US/09/965,528  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/134,949  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/144,270  
; PRIOR FILING DATE: 1999-07-15  
; PRIOR APPLICATION NUMBER: 60/146,700  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: 60/157,508  
; PRIOR FILING DATE: 1999-10-04  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PERL Program  
; SEQ ID NO 16  
; LENGTH: 178  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20020187523A1 5037143CD1  
US-09-965-528-16

Query Match 100.0%; Score 964; DB 9; Length 178;  
Best Local Similarity 100.0%; Pred. No. 2.9e-72;  
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MAAARLCLSLLLSTCVALLQPLLGAGAPLEVPVPGDNATPEQMAQYAADLRRYINML 60
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Db 61 TRPCVPQLGREIPAPGTLPGHITLSPAPAPAPSRPALGKTGHLCTGLDQCALGK 120
Qy 121 MVPTGRYETGGLAPGHSACPCCLPPPRYGRKHEDTLAFSEWGSPhAAVPRELSPLDL 178
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RESULT 2
US-10-002-048A-2
; Sequence 2, Application US/09757712
; Publication No. US20010016339A1
; GENERAL INFORMATION:
; APPLICANT: SOUTHAN, CHRISTOPHER
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30015-C1
; CURRENT APPLICATION NUMBER: US/09/757,712
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: EP 97307187.1
; PRIOR FILING DATE: 1997-09-16
; PRIOR APPLICATION NUMBER: 09/110,715
; PRIOR FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 95
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-757-712-2

Query Match 39.3%; Score 378.5; DB 10; Length 95;
Best Local Similarity 47.2%; Pred. No. 1.5e-24;
Matches 84; Conservative 4; Mismatches 7; Indels 83; Gaps 1;

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Db 61 TR----- 62
Qy 121 MVPTGRYETGGLAPGHSACPCCLPPPRYGRKHEDTLAFSEWGSPhAAVPRELSPLDL 178
Db 63 -----HRYGRDKEDTLAFSEWGSPhAAVPRELSPLDL 95

RESULT 3
US-10-016-969-1
; Sequence 1, Application US/10016969
; Patent No. US20020141985A1
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Pittner, Richard
; APPLICANT: Young, Andrew
; APPLICANT: Paterniti, James
; TITLE OF INVENTION: Peptide YY and Peptide YY Agonists for the Treatment of Metabolic
; FILE REFERENCE: 24001-010
; CURRENT APPLICATION NUMBER: US/10/016,969
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/256,216
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-016-969-1

Query Match 19.3%; Score 186; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 APLPEVPVPGDNATPEQMAQYAADLRRYINMLTRPR 64
Db 1 APLPEVPVPGDNATPEQMAQYAADLRRYINMLTRPR 35

RESULT 4
US-10-002-048A-2
; Sequence 2, Application US/10002048A
; Publication No. US20020182616A1
; GENERAL INFORMATION:
; APPLICANT: Wahlestedt, Claes
; APPLICANT: Ding, Bo
; TITLE OF INVENTION: Single Nucleotide Polymorphisms
; FILE REFERENCE: 10806-143
; CURRENT APPLICATION NUMBER: US/10/002,048A
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: SE 0004035-2
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 97
; TYPE: PRT
; ORGANISM: human
US-10-002-048A-2

Query Match 10.7%; Score 103.5; DB 9; Length 97;
Best Local Similarity 39.1%; Pred. No. 0.056;
Matches 25; Conservative 12; Mismatches 18; Indels 9; Gaps 2;

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Qy 61 TRPR 64
Db 60 TRQR 63

RESULT 5
US-09-737-149-2
; Sequence 2, Application US/09737149
; Patent No. US20020077466A1
; GENERAL INFORMATION:
; APPLICANT: Spaderna, Steven K
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Muralidhara, Padigaru
; APPLICANT: Spytek, Kimberly A.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-620 CIP
; CURRENT APPLICATION NUMBER: US/09/737,149
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/170,564
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: 60/173,165
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: 60/173,362
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: 60/173,544
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/174,404
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 60/174,962
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 60/223,929
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; PRIOR FILING DATE: 2000-08-09
;
; NUMBER OF SEQ ID NOS: 49
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; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 2
;
; LENGTH: 3014
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; TYPE: PRT
;
; ORGANISM: Homo sapiens
US-09-737-149-2

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Query Match	10.6%	Score 102;	DB 10;	Length 3014;
Best Local Similarity	29.3%;	Pred. No. 3.7;		
Matches	49; Conservative	9; Mismatches	63; Indels	46; Gaps
Qy	10	LILLSTCVALLQLLGAQGAPLEVPYFGDNATPEQAQVAADLRYYINMLTRPCVPO.	69	
	:	:   :	:	:
Dd	12	LLLELAAL---PAMGLRAAAWEPRVGGR-----AFALRPCCTYAVGAACTPRA	60	
	:	:   :	:	:
Qy	70	GREIPAGPTLG-----ELHIFGHTLSPAPAPASR-----PALGKTGHL	108	
	:	:::	:	:
b	61	PRELLDVGRDRLAGRRRVSGAGRPPLQVRIVARSAPTALSRLRARTHTLPGCGARAL	120	
	:	:	:	:
Qy	109	CSTGLDQC-ALGHMVTGTRETGGIAPG-HSA-----CPCCLFPPR	147	
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Dd	121	CGTGABLCGALCFPPV-----GGCAAAQHSAALAAPTTLPACRCPPR	161	
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RESULT 6
US-10-016-969-2
; Sequence 2, Application US/10016969
; Patent No. US20020141985A1
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Pittner, Richard
; APPLICANT: Young, Andrew
; APPLICANT: Paterniti, James
; TITLE OF INVENTION: Peptide YY and Peptide YY agonists for the Treatment of Metabolic
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 24001-010
; CURRENT APPLICATION NUMBER: US/10/016,969
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/256,216
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; 10-016-969-2

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	Query Match	10.3%	Score 99;	DB 12;	Length 36;
	Best Local Similarity	47.1%;	Pred. NO. 0.043;		
	Matches 16;	Conservative 11;	Mismatches 7;	Indels 0;	Gaps 0;
QY	31 PLEVPVPGDNATPEQMAQYAADLRYYINMLTRP	64			
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RESULT 7  
US-10-038-045-4  
; Sequence 4, Application US/10038045  
; Patent No. US20020150964A1  
; GENERAL INFORMATION:  
; APPLICANT: Mor, Amram  
; Vouldoukis, Ioannis  
; Nicolas, Pierre  
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas

```

; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/038,045
; FILING DATE: 02-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/181,941
; FILING DATE: 28-Oct-1998
; APPLICATION NUMBER: US 08/574,701
; FILING DATE: 19-Dec-1995
; APPLICATION NUMBER: FR 95 07831
; FILING DATE: 29-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3909-0021-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20020150964A1
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-038-045-4

Query Match      10.3%; Score 99; DB 12; Len
Best Local Similarity 47.1%; Pred. No. 0.043;
Matches 16; Conservative 11; Mismatches 7; I

Qy   31 PLEPVVGDNTPEOMAQYADLRRLNYMLTRPR 64
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Db   2 PAKPEAPGEDASPELSRYASLHLYNLVTQR 35

RESULT 8
US-10-038-045-2
; Sequence 2, Application US/10038045
; Patent No. US20020150964A1
; GENERAL INFORMATION:
; APPLICANT: Moram, Amram
; Vouldoukis, Ioannis
; Nicolas, Pierre
; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
; OF THE IMMUNE SYSTEM IN HUMANS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/038,045
; FILING DATE: 02-Jan-2002

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APPLICANT: Mor, Amram  
Vouldoukis, Ioannis  
Nicolas, Pierre  
TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/038,045  
FILING DATE: 02-Jan-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/181,941  
FILING DATE: 28-Oct-1998  
APPLICATION NUMBER: US 08/574,701  
FILING DATE: 19-DEC-1995  
APPLICATION NUMBER: FR 95 07831  
FILING DATE: 29-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 3909-0021-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5656  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. US20020150964A1e  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-038-045-3

Query Match 9.2%; Score 89; DB 12; Length 36;  
Best Local Similarity 50.0%; Pred. No. 0.28;  
Matches 17; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

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Db 2 PSKPDNFGDAPADMAKYALRHYINLITRQR 35

Search completed: March 1, 2003, 09:17:19  
Job time : 16 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2003, 09:11:46 ; Search time 143 Seconds  
(without alignments)  
802.535 Million cell updates/sec

Title: US-09-965-528-16

Perfect score: 964

Sequence: 1 MAARLCLSLLSTCVALL.....FSEWGSPHAAPRELSPDL 178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents\_AA\_Main.\*

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2: /cgn2_6/ptodata/1/paa/US06_COMB.pcp.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pcp.*
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6: /cgn2_6/ptodata/1/paa/US082_COMB.pcp.*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pcp.*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pcp.*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pcp.*
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27: /cgn2_6/ptodata/1/paa/US60_COMB.pcp.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	964	100.0	178	23	US-09-965-528-16
2	964	100.0	178	23	US-09-979-300-16
3	964	100.0	178	27	US-60-144-270-6
4	441.5	45.8	95	25	US-10-177-488-86
5	379.3	39.3	87	27	US-60-200-109-982
6	378.5	39.3	95	15	US-09-110-715-2

7	378.5	39.3	95	21	US-09-757-712-2	Sequence 2, Appli
8	378.5	39.3	95	24	US-10-036-657-32	Sequence 32, Appl
9	356	36.9	94	27	US-60-200-109-981	Sequence 981, App
10	311	32.3	64	27	US-60-196-718-4967	Sequence 4967, Ap
11	310.5	32.2	92	27	US-60-192-739-3324	Sequence 3324, Ap
12	310.5	32.2	92	27	US-60-194-243-2397	Sequence 2397, Ap
13	186	19.3	36	1	PCT-US02-30533-25	Sequence 25, Appl
14	186	19.3	36	20	US-09-657-276-391	Sequence 391, App
15	186	19.3	36	24	US-10-016-969-1	Sequence 1, Appl
16	186	19.3	38	1	PCT-US02-22821-112	Sequence 112, App
17	186	19.3	38	25	US-10-197-954-112	Sequence 112, App
18	182	18.9	36	1	PCT-US02-30533-28	Sequence 28, Appl
19	182	18.9	36	27	US-60-196-718-4968	Sequence 4968, Ap
20	177	18.4	36	1	PCT-US02-30533-26	Sequence 26, Appl
21	177	18.4	36	1	PCT-US02-30533-27	Sequence 27, Appl
22	176	18.3	36	1	PCT-US02-30533-29	Sequence 29, Appl
23	174	18.0	33	27	US-60-195-053-1911	Sequence 1911, Ap
24	169.5	17.6	37	1	PCT-US02-30533-32	Sequence 32, Appl
25	168	17.4	36	1	PCT-US02-30533-3	Sequence 3, Appli
26	162	16.8	32	27	US-60-195-053-1467	Sequence 1467, Ap
27	154	16.0	36	1	PCT-US02-30533-31	Sequence 31, Appl
28	139	14.4	36	1	PCT-US02-30533-30	Sequence 30, Appl
29	139	14.4	36	20	US-09-657-276-395	Sequence 395, App
30	123	12.8	36	1	PCT-US02-30533-35	Sequence 35, Appl
31	114	11.8	36	20	US-09-657-276-394	Sequence 394, App
32	113	11.7	36	1	PCT-US02-30533-11	Sequence 11, Appl
33	110	11.4	36	20	US-09-657-276-400	Sequence 400, App
34	109	11.3	97	18	US-09-499-526-3	Sequence 3, Appli
35	109	11.3	176	1	PCT-US00-26524B-6128	Sequence 6128, Ap
36	109	11.3	176	25	US-10-106-698-6138	Sequence 6138, Ap
37	107	11.1	36	20	US-09-657-276-283	Sequence 283, App
38	106	11.0	36	1	PCT-US02-30533-34	Sequence 34, Appl
39	103.5	10.7	97	1	PCT-US00-19666-65	Sequence 65, Appl
40	103.5	10.7	97	1	PCT-US00-34758-3	Sequence 3, Appli
41	103.5	10.7	97	1	PCT-US02-23913-289	Sequence 289, App
42	103.5	10.7	97	13	US-08-994-946-6	Sequence 6, Appli
43	103.5	10.7	97	17	US-09-310-707A-16	Sequence 16, Appl
44	103.5	10.7	97	21	US-09-708-344-7	Sequence 7, Appli
45	103.5	10.7	97	21	US-09-708-344A-7	Sequence 7, Appli

#### ALIGNMENTS

RESULT 1  
US-09-965-528-16  
; Sequence 16, Application US/09965528  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: YUE, Henry  
; APPLICANT: LAL, Preeti  
; APPLICANT: BURFORD, Neil  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: AZIMZAI, Valda  
; APPLICANT: LU, Dying Aina M.  
; APPLICANT: PATTERSON, Chandra  
; TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES  
; FILE REFERENCE: PF-0701 USA  
; CURRENT APPLICATION NUMBER: US/09/965,528  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/134,949  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/144,270  
; PRIOR FILING DATE: 1999-07-15  
; PRIOR APPLICATION NUMBER: 60/146,700  
; PRIOR FILING DATE: 1999-07-30  
; PRIOR APPLICATION NUMBER: 60/157,508  
; PRIOR FILING DATE: 1999-10-04  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PERL Program  
; SEQ ID NO 16

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; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 5037143CD1
US-09-965-528-16

Query Match      100.0%; Score 964; DB 23; Length 178;
Best Local Similarity 100.0%; Pred. No. 5.2e-73;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAARCLSLLLSTCVALLQPLLAGAOGAPLEPVVPGDNATPEQMAQYAADLRRYINML 60
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Db 61 TRPRCVPOLGREIPAPGTGLGPLHPIGHTLSPAPAPAPSPALGKTGHLCTGLDQCALGK 120
QY 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPhAAVPRELSPLDL 178
Db 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPhAAVPRELSPLDL 178

RESULT 2
US-09-979-300-16
; Sequence 16, Application US/09979300
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Extracellular Signaling Molecules
; FILE REFERENCE: [list docket ID here]
; CURRENT APPLICATION NUMBER: US/09/979,300
; CURRENT FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 16
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 5037143CD1
US-09-979-300-16

Query Match      100.0%; Score 964; DB 23; Length 178;
Best Local Similarity 100.0%; Pred. No. 5.2e-73;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAARCLSLLLSTCVALLQPLLAGAOGAPLEPVVPGDNATPEQMAQYAADLRRYINML 60
Db 1 MAAARCLSLLLSTCVALLQPLLAGAOGAPLEPVVPGDNATPEQMAQYAADLRRYINML 60
QY 61 TRPRCVPOLGREIPAPGTGLGPLHPIGHTLSPAPAPAPSPALGKTGHLCTGLDQCALGK 120
Db 61 TRPRCVPOLGREIPAPGTGLGPLHPIGHTLSPAPAPAPSPALGKTGHLCTGLDQCALGK 120
QY 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPhAAVPRELSPLDL 178
Db 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPhAAVPRELSPLDL 178

RESULT 3
US-60-144-270-6
; Sequence 6, Application US/60144270
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Azimzai, Yalda
; TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PF-0720 P
; CURRENT APPLICATION NUMBER: US/60/144,270
; CURRENT FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte Clone No: 5037143
US-60-144-270-6

Query Match      100.0%; Score 964; DB 27; Length 178;
Best Local Similarity 100.0%; Pred. No. 5.2e-73;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAAARCLSLLLSTCVALLQPLLAGAOGAPLEPVVPGDNATPEQMAQYAADLRRYINML 60
QY 61 TRPRCVPOLGREIPAPGTGLGPLHPIGHTLSPAPAPAPSPALGKTGHLCTGLDQCALGK 120
Db 61 TRPRCVPOLGREIPAPGTGLGPLHPIGHTLSPAPAPAPSPALGKTGHLCTGLDQCALGK 120
QY 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPhAAVPRELSPLDL 178
Db 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPhAAVPRELSPLDL 178

RESULT 4
US-10-177-488-86
; Sequence 86, Application US/10177488
; GENERAL INFORMATION:
; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koeppe, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1 US
; CURRENT APPLICATION NUMBER: US/10/177,488
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/300,880
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/304,813
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/312,312
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 60/314,280
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/339,227
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/336,827
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/378,885
; PRIOR FILING DATE: 2002-05-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 86
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-177-488-86

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Best Local Similarity 53.4%; Pred. No. 3.2e-29;
Matches 95; Conservative 0; Mismatches 0; Indels 83; Gaps 1;

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Db 1 MAAARCLSLLLSTCVALLQPLLGAGAPLEPVPGDNATPEQMAQYAADLRRYINML 60

QY 61 TRPCVQPLGREIPAPGTLPGHLSPPAPAPSRPALGKTGHLCTGLDQCALGK 120
Db 61 TR----- 62

121 MVPTGRYETGGLAPGHSACPCCLFPFRYKGRHKEDTLAFSEWGSPPHAAVPRELSPLDL 178
Db 63 -----PRYKGRHKEDTLAFSEWGSPPHAAVPRELSPLDL 95

RESULT 5
US-60-200-109-982
; Sequence 982, Application US/60200109
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL000484
; CURRENT APPLICATION NUMBER: US/60/200,109
; CURRENT FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 1348
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 982
; LENGTH: 87
; TYPE: PRT
; ORGANISM: HUMAN
US-60-200-109-982

Query Match 39.3%; Score 379; DB 27; Length 87;
Best Local Similarity 50.3%; Pred. No. 5.5e-24;
Matches 86; Conservative 0; Mismatches 1; Indels 84; Gaps 2;

1 MAAARCLSLLLSTCVALLQPLLGAGAPLEPVPGDNATPEQMAQYAADLRRYINML 60
1 MAAARCLSLLLSTCVALLQPLLGAGAPLEPVPGDNATPEQMAQYAADLRRYINML 60

61 TRPCVQPLGREIPAPGTLPGHLSPPAPAPSRPALGKTGHLCTGLDQCALGK 120
61 TR----- 62

121 MVPTGRYETGGLAPGHSACPCCLFPFRYKGRHKEDTLAFSEWGSPPHAAVPR 171
Db 63 -----PRYKGRHKEDTLAFS-GGSPHAAVPR 87

RESULT 6
US-09-110-715-2
; Sequence 2, Application US/09110715
; GENERAL INFORMATION:
; APPLICANT: SOUTHAN, CHRISTOPHER
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA

Query Match 39.3%; Score 378.5; DB 21; Length 95;
Best Local Similarity 47.2%; Pred. No. 6.7e-24;
Matches 84; Conservative 4; Mismatches 7; Indels 83; Gaps 1;
```

```
;
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/110,715
; FILING DATE: 07-JULY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 97307187.1
; FILING DATE: 16-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-110-715-2

Query Match 39.3%; Score 378.5; DB 15; Length 95;
Best Local Similarity 47.2%; Pred. No. 6.7e-24;
Matches 84; Conservative 4; Mismatches 7; Indels 83; Gaps 1;

QY 1 MAAARCLSLLLSTCVALLQPLLGAGAPLEPVPGDNATPEQMAQYAADLRRYINML 60
Db 1 MAAARCLSLLLSTCVALLQPLLGAGAPLEPVPGDNATPEQMAQYAADLRRYINML 60

QY 61 TRPCVQPLGREIPAPGTLPGHLSPPAPAPSRPALGKTGHLCTGLDQCALGK 120
Db 61 TR----- 62

121 MVPTGRYETGGLAPGHSACPCCLFPFRYKGRHKEDTLAFSEWGSPPHAAVPRELSPLDL 178
Db 63 -----HRYGERKEDTLAFSEWGSPPHAAVPRELSPLDL 95

RESULT 7
US-09-757-712-2
; Sequence 2, Application US/09757712
; GENERAL INFORMATION:
; APPLICANT: SOUTHAN, CHRISTOPHER
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30015-C1
; CURRENT APPLICATION NUMBER: US/09/757,712
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: EP 97307187.1
; PRIOR FILING DATE: 1997-09-16
; PRIOR APPLICATION NUMBER: 09/110,715
; PRIOR FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 95
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-757-712-2

Query Match 39.3%; Score 378.5; DB 21; Length 95;
Best Local Similarity 47.2%; Pred. No. 6.7e-24;
Matches 84; Conservative 4; Mismatches 7; Indels 83; Gaps 1;

QY 1 MAAARCLSLLLSTCVALLQPLLGAGAPLEPVPGDNATPEQMAQYAADLRRYINML 60
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Db 1 MAAACRCLSLLLSTCVALLQPLLGARGAPLEPLYPGDNTPPEQMAQYTAELRRYINML 60  
QY 61 TRPRCVPOLGREIPAPGTGLPHIPGHTLSPAPAPSRPALGKTGHLCTGLDQCALGK 120  
Db 61 TR-----62  
QY 121 MVPTGRYETGGLAPGHSACPCCLFPFPRYGRKHEDTLAFSEWGSPPHAAVPR-ELSP 175  
Db 63 -----PRYGRKHEDTLAFSEWGSPPHAAVPR-ELSP 93

RESULT 8  
US-10-036-657-32  
; Sequence 32, Application US/10036657  
; GENERAL INFORMATION:  
; APPLICANT: Earl Francis Albone, et al.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES  
; FILE REFERENCE: GP-70778B-C1  
; CURRENT APPLICATION NUMBER: US/10/036,657  
; CURRENT FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-10-036-657-32

Query Match 39.3%; Score 378.5; DB 24; Length 95;  
Best Local Similarity 47.2%; Pred. No. 6.7e-24;  
Matches 84; Conservative 4; Mismatches 7; Indels 83; Gaps 1;

QY 1 MAAARCLSLLLSTCVALLQPLLGARGAPLEPLYPGDNTPPEQMAQYAADLRRYINML 60  
Db 1 MAAACRCLSLLLSTCVALLQPLLGARGAPLEPLYPGDNTPPEQMAQYTAELRRYINML 60  
QY 61 TRPRCVPOLGREIPAPGTGLPHIPGHTLSPAPAPSRPALGKTGHLCTGLDQCALGK 120  
Db 61 TR-----62

QY 121 MVPTGRYETGGLAPGHSACPCCLFPFPRYGRKHEDTLAFSEWGSPPHAAVPR-ELSP 178  
Db 63 -----HRYGRDKEDTLAFSEWGSPPHAAVPR-ELSP 95

RESULT 9  
US-60-200-109-981  
; Sequence 981, Application US/60200109  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND  
; FILE REFERENCE: CL000484  
; CURRENT APPLICATION NUMBER: US/60/200,109  
; CURRENT FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 1348  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 981  
; LENGTH: 94  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-60-200-109-981

Query Match 36.9%; Score 356; DB 27; Length 94;  
Best Local Similarity 46.6%; Pred. No. 5.2e-22;  
Matches 82; Conservative 2; Mismatches 8; Indels 84; Gaps 2;

QY 1 MAAARCLSLLLSTCVALLQPLLGARGAPLEPLYPGDNTPPEQMAQYAADLRRYINML 60  
Db 1 MAAACRCLSLLLSTCVALLQPLLGARGAPLEPLYPGDNTPPEQMAQYTAELRRYINML 60

QY 61 TRPRCVPOLGREIPAPGTGLPHIPGHTLSPAPAPSRPALGKTGHLCTGLDQCALGK 120  
Db 61 TR-----62  
QY 121 MVPTGRYETGGLAPGHSACPCCLFPFPRYGRKHEDTLAFSEWGSPPHAAVPR-ELSP 175  
Db 63 -----PRYGRKHEDTLAFSEWGSPPHAAVPR-ELSP 93

RESULT 10  
US-60-196-718-4967  
; Sequence 4967, Application US/60196718  
; GENERAL INFORMATION:  
; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND  
; FILE REFERENCE: CL000456  
; CURRENT APPLICATION NUMBER: US/60/196,718  
; CURRENT FILING DATE: 2000-04-13  
; NUMBER OF SEQ ID NOS: 7494  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4967  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-60-196-718-4967

Query Match 32.3%; Score 311; DB 27; Length 64;  
Best Local Similarity 96.9%; Pred. No. 2.1e-18;  
Matches 62; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAARCLSLLLSTCVALLQPLLGARGAPLEPLYPGDNTPPEQMAQYAADLRRYINML 60  
Db 1 MAAARCLSLLLSTCVALLQPLLGARGAPLEPLYPGDNTPPEQMAQYAADLRRYINML 60  
QY 61 TRPR 64  
Db 61 TRPR 64

RESULT 11  
US-60-192-739-3324  
; Sequence 3324, Application US/60192739  
; GENERAL INFORMATION:  
; APPLICANT: Bonazzi, Vivien  
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND  
; FILE REFERENCE: CL000406  
; CURRENT APPLICATION NUMBER: US/60/192,739  
; CURRENT FILING DATE: 2000-03-28  
; NUMBER OF SEQ ID NOS: 4532  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3324  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(92)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-60-192-739-3324

Query Match 32.2%; Score 310.5; DB 27; Length 92;  
Best Local Similarity 40.6%; Pred. No. 3.5e-18;  
Matches 71; Conservative 5; Mismatches 16; Indels 83; Gaps 1;

QY 2 AARCLSLLLSTCVALLQPLLGARGAPLEPLYPGDNTPPEQMAQYAADLRRYINMLT 61  
Db 1 AAACRCLSLLLSTCVALLQPLLGARGAPLEPLYPGDNTPPEQMAQYTAELRRYINMLT 60  
QY 62 RPRCVPOLGREIPAPGTGLPHIPGHTLSPAPAPSRPALGKTGHLCTGLDQCALGKM 121

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Query Match      19.3%; Score 186; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14  
US-09-657-276-391  
; Sequence 391, Application US/09657276  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibadeau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS

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: NUMBER OF SEQ ID NOS: 1617
:
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 391
: LENGTH: 36
: TYPE: PRT
: ORGANISM: Artificial Sequence
:
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: Peptide
: US-09-657-276-391

```

```

RESULT 15
US-10-016-969-1
; Sequence 1, Application US/10016969
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Pittner, Richard
; APPLICANT: Young, Andrew
; APPLICANT: Paterniti, James
; TITLE OF INVENTION: Peptide YY and Peptid
; FILE REFERENCE: 24001-010
; CURRENT APPLICATION NUMBER: US/10/016,969-1
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/256,216
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-969-1

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:12:05 ; Search time 25 Seconds  
(without alignments)  
663.560 Million cell updates/sec

**Title:** US-09-965-528-16

Perfect score: 964  
Sequence: 1 MAAARLCLSLLLSTCVALL.....FSEWGSPHAAVPRELSPLDL 178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 494224 seqs, 93196565 residues

total number of hits satisfying chosen parameters: 4942224

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 s

Database : Pending Patents AA New: \*

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1: /cgn2_6/ptodata2/paa/PCT_NEW_COMB.pcp.*
2: /cgn2_6/ptodata2/paa/US06_NEW_COMB.pcp.*
3: /cgn2_6/ptodata2/paa/US07_NEW_COMB.pcp.*
4: /cgn2_6/ptodata2/paa/US08_NEW_COMB.pcp.*
5: /cgn2_6/ptodata2/paa/US09_NEW_COMB.pcp.*
6: /cgn2_6/ptodata2/paa/US10_NEW_COMB.pcp.*
7: /cgn2_6/ptodata2/paa/US16_NEW_COMB.pcp.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	186	19.3	36	1	PCT-US02-31944A-25	Sequence 25, Appl
2	186	19.3	36	1	PCT-US02-30533A-25	Sequence 25, Appl
3	182	18.9	36	1	PCT-US02-31944A-28	Sequence 28, Appl
4	182	18.9	36	1	PCT-US02-30533A-28	Sequence 28, Appl
5	177	18.4	36	1	PCT-US02-31944A-26	Sequence 26, Appl
6	177	18.4	36	1	PCT-US02-31944A-27	Sequence 27, Appl
7	177	18.4	36	1	PCT-US02-30533A-26	Sequence 26, Appl
8	177	18.4	36	1	PCT-US02-30533A-27	Sequence 27, Appl
9	176	18.3	36	1	PCT-US02-31944A-29	Sequence 29, Appl
10	176	18.3	36	1	PCT-US02-30533A-29	Sequence 29, Appl
11	169.5	17.6	37	1	PCT-US02-31944A-32	Sequence 32, Appl
12	169.5	17.6	37	1	PCT-US02-30533A-32	Sequence 32, Appl
13	168	17.4	36	1	PCT-US02-31944A-3	Sequence 3, Appl
14	168	17.4	36	1	PCT-US02-30533A-3	Sequence 3, Appl
15	154	16.0	36	1	PCT-US02-31944A-31	Sequence 31, Appl
16	154	16.0	36	1	PCT-US02-30533A-31	Sequence 31, Appl
17	139	14.4	36	1	PCT-US02-31944A-30	Sequence 30, Appl
18	139	14.4	36	1	PCT-US02-30533A-30	Sequence 30, Appl
19	123	12.8	36	1	PCT-US02-31944A-35	Sequence 35, Appl
20	123	12.8	36	1	PCT-US02-30533A-35	Sequence 35, Appl
21	122	12.7	36	6	US-10-072-012-875	Sequence 875, App
22	116	12.0	98	6	US-10-072-012-710	Sequence 710, App
23	113	11.7	36	1	PCT-US02-31944A-11	Sequence 11, Appl
24	113	11.7	36	1	PCT-US02-30533A-11	Sequence 11, Appl
25	109	11.3	90	6	US-10-072-012-712	Sequence 712, App
26	109	11.3	90	6	US-10-072-012-713	Sequence 713, App

Sequence 709, App  
Sequence 711, App  
Sequence 34, App1  
Sequence 34, App1  
Sequence 1630, App  
Sequence 1671, App  
Sequence 1675, App  
Sequence 631, App  
Sequence 107, App  
Sequence 107, App  
Sequence 444, App  
Sequence 14, App1  
Sequence 69, App1  
Sequence 14, App1  
Sequence 69, App1  
Sequence 69, App1  
Sequence 69, App1  
Sequence 69, App1  
Sequence 69, App1

## ALIGNMENTS

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RESULT 1
PCT-US02-31944A-25
; Sequence 25, Application PC/TUS0231944A
; GENERAL INFORMATION:
; APPLICANT: Imperial College Innovations Limited
; APPLICANT: Bloom, Stephen R.
; APPLICANT: Small, Caroline J.
; APPLICANT: Batterham, Rachel L.
; APPLICANT: Ghatel, Mohammad A.
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Modification of Feeding Behavior
; FILE REFERENCE: 895-63727
; CURRENT APPLICATION NUMBER: PCT/US02/31944A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: GB 0200507.2
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 335
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Ovis aries
PCT-US02-31944A-25

```

```
Query Match          19.3%; Score 186; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 30 APLEVPYPGDNATPEQMAQYAADLRRYINMLTRPR 64  
 |||||  
 Db 1 APLEVPYPGDNATPEQMAQYAADLRRYINMLTRPR 35  
 |||||

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RESULT 2
PCF-US02-30533A-25
; Sequence 25, Application PC/TUS0230533A
; GENERAL INFORMATION:
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Assessment Of Neuro

```

```

, FILE REFERENCE: 899-63986
, CURRENT APPLICATION NUMBER: PCT/US02/30533A
, CURRENT FILING DATE: 2002-09-24
, PRIOR APPLICATION NUMBER: US 60/324,406
, PRIOR FILING DATE: 2001-09-24
, PRIOR APPLICATION NUMBER: US 60/392,109
, PRIOR FILING DATE: 2002-06-28
, NUMBER OF SEQ ID NOS: 352
, SOFTWARE: PatencIn version 3.1
, SEQ ID NO 25
, LENGTH: 36
, TYPE: PRT
, ORGANISM: Ovis aries
, PCT-US02-30533A-25

```

```

Query Match      19.3%; Score 186; DB 1; Length 36;
Best Local Similarity 100.0%; Pred.No. 3.8e-07;
Matches 35; Conservative 0; Mismatches 0; Indels

```

```

RESULT 3
PCT-US02-31944A-28
; Sequence 28, Application PC/TUS0231944A
; GENERAL INFORMATION:
; APPLICANT: Imperial College Innovations Limited
; APPLICANT: Bloom, Stephen R.
; APPLICANT: Small, Caroline J.
; APPLICANT: Batterham, Rachel L.
; APPLICANT: Ghatei, Mohammad A.
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Modification of Feeding Behavior
; FILE REFERENCE: 899-63727
; CURRENT APPLICATION NUMBER: PCT/US02/31944A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: GB 0200507.2
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 335
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Felis catus
PCT-US02-31944A-28

```

	Query Match	18.9%	Score 182;	DB 1;	Length 36;
	Best Local Similarity	97.1%	Pred. No. 7.5e-07;		
	Matches 34;	Conservative	1;	Mismatches 0;	Indels
QY	30	APLEPVYPGDNATPEQMAQYAADLRYYINMLTPR	64		
DB	1	APLEPVYPGDNATPEQMAQYAADLRYYINMLTPR	35		

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RESULT 4
PCT-US02-30533A-28
; Sequence 28, Application PC/TUS0230533A
; GENERAL INFORMATION:
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Assessment of Neur

```

```

; FILE REFERENCE: 899-63986
; CURRENT APPLICATION NUMBER: PCT/US02/30533A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Felis catus
; PCT-US02-30533A-28

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Query Match	18.9%;	Score 182;	DB 1;	Length 361
Best Local Similarity	97.1%;	Pred. No. 7.5e-07;		
Matches	34;	Conservative	1;	Mismatches 0; Indels
QY	30	APLEPVVPGDNATPEQMAQVAAALRRYINNLTRPR	64	
Db	1	APLEPVVPGDNATPEQMAQVAAALRRYINNLTRPR	35	

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RESULT 5
PCT-US02-31944A-26
; Sequence 26, Application PC/TUS0231944A
; GENERAL INFORMATION:
; APPLICANT: Imperial College Innovations Limited
; APPLICANT: Bloom, Stephen R.
; APPLICANT: Small, Caroline J.
; APPLICANT: Batterham, Rachel L.
; APPLICANT: Ghaei, Mohammad A.
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Modification of Feeding Behavior
; FILE REFERENCE: 899-63727
; CURRENT APPLICATION NUMBER: PCT/US02/31944A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: GB 0200507.2
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 335
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Sus sp.
; PCT-US02-31944A-26

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Query Match	18.4%	Score 177	DB 1	Length 36
Best Local Similarity	94.3%	Pred. No. 1.8e-06		
Matches	33	Conservative	2	Mismatches 0
				Indels 0
Gaps				0

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RESULT 6
PCT-US02-31944A-27
; Sequence 27, Application PC/TUS0231944A
; GENERAL INFORMATION:
; APPLICANT: Imperial College Innovations Limited
; APPLICANT: Bloom, Stephen R.
; APPLICANT: Small, Caroline J.
; APPLICANT: Batterham, Rachel L.
; APPLICANT: Ghatei, Mohammad A.

```

```
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolin
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Modification of Feeding Behavior
; FILE REFERENCE: 899-63727
; CURRENT APPLICATION NUMBER: PCT/US02/31944A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: GB 0200507.2
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 335
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Canis familiaris
T-US02-31944A-27

Query Match      18.4%; Score 177; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 1.8e-06;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEVPYVPGDNTPEQMAQYAADLRRYINMLTRPR 64
|||||:|||||:|||||:|||||:|||||:|||||
Db 1 APLEVPYVPGDNTPEQMAQYAAELRRYINMLTRPR 35

RESULT 7
PCT-US02-30533A-26
; Sequence 26, Application PC/TUS0230533A
; GENERAL INFORMATION:
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolin
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding Behavior
; FILE REFERENCE: 899-63986
; CURRENT APPLICATION NUMBER: PCT/US02/30533A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Sus sp.
PCT-US02-30533A-26

Query Match      18.4%; Score 177; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 1.8e-06;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEVPYVPGDNTPEQMAQYAADLRRYINMLTRPR 64
|||||:|||||:|||||:|||||:|||||:|||||
Db 1 APLEVPYVPGDNTPEQMAQYAAELRRYINMLTRPR 35

RESULT 8
PCT-US02-30533A-27.
; Sequence 27, Application PC/TUS0230533A
; GENERAL INFORMATION:
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolin
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding Behavior
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; FILE REFERENCE: 899-63986
; CURRENT APPLICATION NUMBER: PCT/US02/30533A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Canis familiaris
PCT-US02-30533A-27

Query Match      18.4%; Score 177; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 1.8e-06;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEVPYVPGDNTPEQMAQYAADLRRYINMLTRPR 64
|||||:|||||:|||||:|||||:|||||:|||||
Db 1 APLEVPYVPGDNTPEQMAQYAAELRRYINMLTRPR 35

RESULT 9
PCT-US02-31944A-29
; Sequence 29, Application PC/TUS0231944A
; GENERAL INFORMATION:
; APPLICANT: Imperial College Innovations Limited
; APPLICANT: Bloom, Stephen R.
; APPLICANT: Small, Caroline J.
; APPLICANT: Batterham, Rachel L.
; APPLICANT: Ghatel, Mohammad A.
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolin
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Modification of Feeding Behavior
; FILE REFERENCE: 899-63727
; CURRENT APPLICATION NUMBER: PCT/US02/31944A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: GB 0200507.2
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 335
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Bos taurus
PCT-US02-31944A-29

Query Match      18.3%; Score 176; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 2.1e-06;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 30 APLEVPYVPGDNTPEQMAQYAADLRRYINMLTRPR 64
|||||:|||||:|||||:|||||:|||||:|||||
Db 1 APLEVPYVPGDNTPEQMAQYAAELRRYINMLTRPR 35

RESULT 10
PCT-US02-30533A-29
; Sequence 29, Application PC/TUS0230533A
; GENERAL INFORMATION:
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolin
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding Behavior
```

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RESULT 12
PCT-US02-30533A-32
; Sequence 32, Application PC/TUS0230533A
; GENERAL INFORMATION:
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Assessment of Neur

```

```

RESULT 14
PCT-US02-30533A-3
; Sequence 3, Application PC/TUS0230533A
; GENERAL INFORMATION:
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Assessment of Neu

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; FILE REFERENCE: 899-63986  
; CURRENT APPLICATION NUMBER: PCT/US02/30533A  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: US 60/324,406  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 60/392,109  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 352  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-30533A-3

Query Match 17.4%; Score 168; DB 1; Length 36;  
Best Local Similarity 91.4%; Pred. No. 8e-06;  
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
Db 30 APLEVPYPGDNATPEQMAQYAADLRRYINMLTRPR 64  
1 ASLEPEYPGDNATPEQMAQYAAELRRYINMLTRPR 35

RESULT 15  
PCT-US02-31944A-31  
; Sequence 31, Application PC/TUS0231944A  
; GENERAL INFORMATION:  
; APPLICANT: Imperial College Innovations Limited  
; APPLICANT: Bloom, Stephen R.  
; APPLICANT: Small, Caroline J.  
; APPLICANT: Batterham, Rachel L.  
; APPLICANT: Gbatei, Mohammad A.  
; APPLICANT: Cowley, Michael  
; APPLICANT: Cone, Roger  
; APPLICANT: Low, Malcolm  
; APPLICANT: Butler, Andrew  
; TITLE OF INVENTION: Modification of Feeding Behavior  
; FILE REFERENCE: 899-63727  
; CURRENT APPLICATION NUMBER: PCT/US02/31944A  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: US 60/324,406  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: GB 0200507.2  
; PRIOR FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: US 60/392,109  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 335  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Mus musculus  
PCT-US02-31944A-31

Query Match 16.0%; Score 154; DB 1; Length 36;  
Best Local Similarity 82.9%; Pred. No. 8.4e-05;  
Matches 29; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
  
QY 30 APLEVPYPGDNATPEQMAQYAADLRRYINMLTRPR 64  
1 ASLEPEYPGDNATPEQMAQYETQLRRYINMLTRPR 35

Search completed: March 1, 2003, 09:16:57  
Job time : 25 secs.



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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:11:12 ; Search time 31 Seconds  
(without alignments)  
168.945 Million cell updates/sec

Title: US-09-965-528-16

Perfect score: 964

Sequence: 1 MAARCLCLLLSTCVALL.....FSEWGSPHAAVPRELPLDL 178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
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5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186	19.3	36	2	US-08-806-203-1
2	103.5	10.7	97	3	US-09-054-393-1
3	103.5	10.7	97	3	US-08-994-946A-6
4	103.5	10.7	97	4	US-09-229-900-1
5	103.5	10.7	97	4	US-09-291-994-6
6	100.5	10.4	505	1	US-08-221-750A-5
7	99	10.3	36	1	US-07-882-923-3
8	99	10.3	36	1	US-08-338-395-1
9	99	10.3	36	1	US-08-338-395-2
10	99	10.3	36	1	US-08-329-151-1
11	99	10.3	36	1	US-08-329-151-2
12	99	10.3	36	3	US-09-054-393-2
13	99	10.3	36	3	US-09-047-986B-1
14	99	10.3	36	3	US-09-047-986B-2
15	99	10.3	36	4	US-09-229-900-2
16	99	10.3	36	4	US-09-181-941-4
17	99	10.3	36	5	PCT-US95-14303-1
18	99	10.3	36	5	PCT-US95-14303-2
19	98.5	10.2	2205	1	US-08-093-453B-2
20	98	10.2	36	1	US-08-329-151-9
21	96.5	10.0	649	4	US-09-192-909-2
22	96	10.0	36	4	US-09-181-941-2
23	94	9.8	36	4	US-09-181-941-1
24	91	9.4	684	1	US-08-555-669-12
25	91	9.4	684	3	US-09-073-663-12
26	89.5	9.3	3033	1	US-07-925-695-5
27	89	9.2	36	1	US-07-882-923-2

28	89	9.2	36	1	US-08-338-395-3	Sequence 3, Appli
29	89	9.2	36	1	US-08-329-151-24	Sequence 24, Appl
30	89	9.2	36	3	US-08-907-403A-1	Sequence 1, Appli
31	89	9.2	36	4	US-09-181-941-3	Sequence 3, Appli
32	89	9.2	36	5	PCT-US95-14303-3	Sequence 3, Appli
33	86	8.9	36	1	US-07-882-923-1	Sequence 1, Appli
34	86	8.9	36	1	US-08-264-030-1	Sequence 1, Appli
35	86	8.9	36	1	US-08-338-395-4	Sequence 4, Appli
36	86	8.9	36	3	US-08-907-403A-2	Sequence 2, Appli
37	86	8.9	36	4	US-09-181-941-5	Sequence 5, Appli
38	86	8.9	36	5	PCT-US95-14303-4	Sequence 4, Appli
39	85	8.8	36	1	US-07-776-272-18	Sequence 18, Appl
40	85	8.8	762	1	US-08-642-255-120	Sequence 120, App
41	85	8.8	762	1	US-08-397-633A-31	Sequence 31, Appl
42	85	8.8	1291	4	US-09-150-460B-10	Sequence 10, Appl
43	85	8.8	1291	4	US-09-220-641-5	Sequence 5, Appli
44	85	8.8	1964	4	US-09-467-997-1	Sequence 1, Appli
45	84	8.7	747	4	US-09-347-878-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1  
US-08-806-203-1  
; Sequence 1, Application US/08806203  
; Patent No. 5830434  
; GENERAL INFORMATION:  
; APPLICANT: TAYLOR, IAN L.  
; APPLICANT: GETTYS, THOMAS  
; TITLE OF INVENTION: METHODS OF TREATING NON-INSULIN  
; TITLE OF INVENTION: DEPENDENT DIABETES MELLITUS WITH  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
; STREET: Suite 1200, 127 Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/806,203  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spratt, Gwendolyn D.  
; REGISTRATION NUMBER: 36,016  
; REFERENCE/DOCKET NUMBER: 19070.0028  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404/688-0770  
; TELEFAX: 404/688-9880  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-806-203-1

Query Match 19.3%; Score 186; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.7e-12;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 APLEPVPGNATPEQMAQYAADLRRYINMLTRPR 64

Db 1 APLEPVPGNATPEQMAQYAADLRRYINMLTRPR 35

```

RESULT 2
US-09-054-393-1
; Sequence 1, Application US/09054393
; Patent No. 6017879
; GENERAL INFORMATION:
; APPLICANT: Mutter, Manfred
; APPLICANT: Lacroix, Jean S.
; APPLICANT: Grouzmann, Eric
; TITLE OF INVENTION: Template Associated NPY Y2-Receptor
; TITLE OF INVENTION: Agonists
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vinson & Elkins LLP
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20004-1008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,393
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: BMR350/48000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)639-6585
; TELEFAX: (202)639-6604
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-09-054-393-1
Query Match          10.7%; Score 103.5; DB 3; Length 97;
Best Local Similarity 39.1%; Pred. No. 0.0025;
Matches 25; Conservative 12; Mismatches 18; Indels 9; Gaps 2;

y      1 MAARLCGLSLLSTCVALLQLLGAQCAPLEVPYPCDNATPQMAYAADLRRYNML 60
       : : ||||| : | : | : | : | : | : | : | : | : | : | : | :
Db     9 LSGLTALSLIV---CLGAL---ABAYPSKPDNPGEDAPEDMARYYGALRHYINLI 59

QY      61 TRPR 64
       |||
Db     60 TRQR 63

RESULT 3
US-08-994-946A-6
; Sequence 6, Application US/08994946A
; Patent No. 6046317
; GENERAL INFORMATION:
; APPLICANT: Koulu, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: A DNA Molecule Encoding a Mutant
; TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

```

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; REFERENCE/DOCKET NUMBER: BMR350/48000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)639-6585
; TELEFAX: (202)639-6604
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-229-900-1

Query Match 10.7%; Score 103.5; DB 4; Length 97;
Best Local Similarity 39.1%; Pred. No. 0.0025;
Matches 25; Conservative 12; Mismatches 18; Indels 9; Gaps 2;

1 MAARCLCLSLLLSTCVALLQLLGAQGAAPLEVPYVPGDNATPEQMAQYAADLRRYINML 60
Db 9 LSGLTALSLLV---CLGAL---AEAYPSKPDNPGEDAPADMARYSALRHYINLI 59

QY 61 TRPR 64
Db 60 TRQR 63

RESULT 5
US-09-291-994-6
; Sequence 6, Application US/09291994
; Patent No. 6312898
; GENERAL INFORMATION:
; APPLICANT: Koulou, Markku
; APPLICANT: Karvonen, Matti
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Uusitupa, Matti
; TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
; TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine
; TITLE OF INVENTION: 7 to Proline 7 Polymorphism in the Prepro-Neuropeptide
; FILE REFERENCE: 2328-112.A
; CURRENT APPLICATION NUMBER: US/09/291.994
; CURRENT FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-291-994-6

Query Match 10.7%; Score 103.5; DB 4; Length 97;
Best Local Similarity 39.1%; Pred. No. 0.0025;
Matches 25; Conservative 12; Mismatches 18; Indels 9; Gaps 2;

1 MAARCLCLSLLLSTCVALLQLLGAQGAAPLEVPYVPGDNATPEQMAQYAADLRRYINML 60
Db 9 LSGLTALSLLV---CLGAL---AEAYPSKPDNPGEDAPADMARYSALRHYINLI 59

QY 61 TRPR 64
Db 60 TRQR 63

RESULT 6
US-08-221-750A-5
; Sequence 5, Application US/08221750A
; Patent No. 5643747
; GENERAL INFORMATION:
; APPLICANT: Baker, Steven M.
; APPLICANT: Deich, Robert A.
; TITLE OF INVENTION: Genes for the Export of Pertussis
```

```
; TITLE OF INVENTION: Holotoxin
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,750A
; FILING DATE: 31-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,619
; FILING DATE: 15-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Alice O.
; REGISTRATION NUMBER: 33,542
; REFERENCE/DOCKET NUMBER: ACC93-01A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 505 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-221-750A-5

Query Match 10.4%; Score 100.5; DB 1; Length 505;
Best Local Similarity 27.5%; Pred. No. 0.04;
Matches 55; Conservative 14; Mismatches 70; Indels 61; Gaps 11;

QY 1 MAARCLCLSLLLSTCVALLQLLGAQGAAPLEVPYVPGDNATPEQMAQYAADLRRYI 57
Db 333 MLAATLCAT---ATLMLTLVPLASSVAGLRRLWP---NAAHPGLAQAHQAARQYA 386
QY 58 NMLTRPCVPLGREIPAPGTLGLPHIPGHTLSPAPAPSPRPAALGKTGKTLCTGLDOCA 117
Db 387 R-----RPAAMAAAAGHOAGTYAASATPAPAPAPSPFPAH-----AYRQYA 430
QY 118 L-GKMVPTG-----RYETGGLAPGHSACPCCLFP-----PRYKG 150
Db 431 LGGARSAPGCDATTGPRRRRTDGFPP---ANPTCHDPRTFQRIAMGHPGHRPHAR 487
QY 151 RHKEDTLAFSEWGSPPAAVP 170
Db 488 RLR-----PEAGRPPACRIP 501

RESULT 7
US-07-882-923-3
; Sequence 3, Application US/07882923
; Patent No. 5328899
; GENERAL INFORMATION:
; APPLICANT: Boublik, Jaroslav H.
; APPLICANT: Rivier, Jean E.F.
; APPLICANT: Brown, Marvin R.
; APPLICANT: Scott, Neal A.
; TITLE OF INVENTION: NPY PEPTIDE ANALOGS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 4250 Executive Square, Suite 510
; CITY: La Jolla
; STATE: CA
```





```
;
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-054-393-2

Query Match 10.3%; Score 99; DB 3; Length 36;
Best Local Similarity 47.1%; Pred. No. 0.002;
Matches 16; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Qy 31 PLEPVYGDNATPEQMAQYAADLRRYINMLTRPR 64
|::| |::| |::| |::| |::| |::| |::| |
Db 2 PIKPEAFGEDASPEELNRYASLRHYLNLVTRQR 35

RESULT 13
US-09-047-986B-1
; Sequence 1, Application US/09047986B
; Patent No. 6046167
GENERAL INFORMATION:
APPLICANT: Balasubramanian, Ambikaipakan
TITLE OF INVENTION: PEPTIDE YY ANALOGS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frost & Jacobs, L.L.P.
STREET: 2500 PNC Center, 201 East Fifth St.
CITY: Cincinnati
STATE: OH
COUNTRY: USA
ZIP: 45202-4182
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,986B
FILING DATE: 25 March 1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kristyne A. Bullock
REGISTRATION NUMBER: 42,371
REFERENCE/DOCKET NUMBER: 9183030/508
TELEPHONE: (513) 651-6731
TELEFAX: (513) 651-6981
TELEX: 21-4396 F&J Cin
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-047-986B-2

Query Match 10.3%; Score 99; DB 3; Length 36;
Best Local Similarity 47.1%; Pred. No. 0.002;
Matches 16; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Qy 31 PLEPVYGDNATPEQMAQYAADLRRYINMLTRPR 64
|::| |::| |::| |::| |::| |::| |
Db 2 PIKPEAFGEDASPEELNRYASLRHYLNLVTRQR 35

RESULT 15
US-09-229-900-2
; Sequence 2, Application US/09229900
; Patent No. 6288029
GENERAL INFORMATION:
APPLICANT: Mutter, Manfred
APPLICANT: Lacroix, Jean S.
APPLICANT: Grouzmann, Eric
TITLE OF INVENTION: Template Associated NPY Y2-Receptor
TITLE OF INVENTION: Agonists
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins LLP
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20004-1008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,900
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BMR350/48000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)639-6585
```



Search completed: March 1, 2003, 09:13:57  
Job time : 33 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:11:12 ; Search time 30 Seconds  
(without alignments)  
1222.546 Million cell updates/sec

Title: US-09-965-528-16  
Perfect score: 964  
Sequence: 1 MAARLCUSLLSTCVALL.....FSEWGSPHAAPVRELPLDL 178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Description
1	169	17.5	Q9gk10 sus scrofa
2	115.5	12.0	Q9i9d3 ictalurus p
3	113.5	11.8	Q9ixd0 mus musculu
4	111	11.5	Q68872 myxococcus
5	110.5	11.5	Q925v2 mus musculu
6	110.5	11.5	Q90wf4 paralichthy
7	106	11.0	Q8spf7 ovis aries
8	105	10.9	Q9xsw6 macaca mula
9	105	10.9	Q90wf3 paralichthy
10	104.5	10.8	Q9tsi6 ovis aries
11	104	10.8	Q9pw68 typhlonecte
12	102.5	10.6	O52861 bacillus su
13	102	10.6	Q9kr9 streptomyce
14	102	10.6	Q9nyq6 homo sapien
15	101	10.5	Q9dgr7 cyprinus ca
16	97.5	10.1	O32062 bacillus su

17	96.5	10.0	2129	12	Q9J6K9	Q9J6K9 rubella vir
18	95.5	9.9	2115	12	Q86500	Q86500 rubella vir
19	95	9.9	36	6	Q9TR93	Q9TR93 oryctolagus
20	95	9.9	1203	4	Q9UMQ7	Q9UMQ7 homo sapien
21	95	9.9	1203	4	Q9Y3Q4	Q9Y3Q4 homo sapien
22	95	9.9	1838	5	Q960G3	Q960G3 drosophila
23	94.5	9.8	2116	12	Q99IE7	Q99IE7 rubella vir
24	94.5	9.8	2116	12	Q99IE5	Q99IE5 rubella vir
25	94.5	9.8	2116	12	Q8VALL	Q8VALL rubella vir
26	94	9.8	301	5	Q9XUT4	Q9XUT4 caenorhabdi
27	94	9.8	545	4	Q9NX25	Q9NX25 homo sapien
28	94	9.8	1400	4	Q9NZ71	Q9NZ71 homo sapien
29	94	9.8	1790	5	Q9VUH6	Q9VUH6 drosophila
30	93.5	9.7	572	3	Q9PAV1	Q9PAV1 candida boi
31	93.5	9.7	893	4	Q9Y2G1	Q9Y2G1 homo sapien
32	93.5	9.7	1111	4	Q9PIQ6	Q9PIQ6 homo sapien
33	93.5	9.7	2116	12	Q8VAL3	Q8VAL3 rubella vir
34	93	9.6	702	11	Q9JME1	Q9JME1 mus musculu
35	93	9.6	774	16	Q9L0Z1	Q9L0Z1 streptomyce
36	93	9.6	854	11	Q9QZS8	Q9QZS8 mus musculu
37	93	9.6	1161	4	Q9UPR4	Q9UPR4 homo sapien
38	92.5	9.6	97	13	Q90WF2	Q90WF2 paralichthy
39	92.5	9.6	675	11	Q9LYM9	Q9LYM9 mus musculu
40	92.5	9.6	1123	11	Q9BDS5	Q9BDS5 mus musculu
41	92.5	9.6	1712	10	Q9AXN1	Q9AXN1 botryocodi
42	92.5	9.6	2116	12	O40955	O40955 rubella vir
43	92.5	9.6	2344	5	Q9N3Y8	Q9N3Y8 caenorhabdi
44	91.5	9.5	577	10	Q9STP1	Q9STP1 arabidopsis
45	91	9.4	295	5	Q20927	Q20927 caenorhabdi

#### ALIGNMENTS

#### RESULT 1

ID	Q9GK10	PRELIMINARY;	PRT;	59 AA.
AC	Q9GK10;			
DT	01-MAR-2001 (Tremblrel. 16, Created)			
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)			
DT	01-MAR-2002 (Tremblrel. 20, Last annotation update)			
DE	Pancreatic polypeptide (Fragment).			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Han X.G., Tsch B.E.;			
RT	"Partial porcine pancreatic polypeptide cDNA sequence (3'end).";			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
CC	-!- SIMILARITY: BELONGS TO THE NPY / PPY / PPY / PPY FAMILY.			
DR	EMBL; AF203915; AAC35647.1; -.			
DR	HSSP; P01302; IBBA.			
DR	InterPro; IPR001955; Pancreatic_hormn.			
DR	Pfam; PF00159; hormone3; 1.			
DR	SMART; SM00309; PAH; 1.			
DR	PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.			
DR	PROSITE; PS00276; PANCREATIC_HORMONE_2; 1.			
KW	Amidation.			
FT	NON TER			
SQ	SEQUENCE 59 AA; 6683 MW; 9A199783B9E29FCD CRC64;			
Query Match				
Best Local Similarity 17.5%; Score 169; DB 6; Length 59;				
Matches 44; Conservative 5; Mismatches 8; Indels 84; Gaps 2;				
Qy	36	YFGDNATPEQMAVAADLRRYINMLTRPCVPQLGREIPAPGTLGPHIPIGHTLSPAPAP 95		
		:     :     :     :		
Db	1	YFGDDATPEQMAVAADLRRYINMLTR----- 27		
Qy	96	APSPALGKTHLSTGLDQCALGKVMPTGRYETGGTGLAPGHSACPCCLFPFRYCKRHED 155		
		:     :     :     :		

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Db 28 -----PRYGRDEED 37
Qy 156 TLFSEWGSPHAAVPRELSPL 176
Db 38 LLDL-KCSLHAAAPRELSPL 57

RESULT 2
Q919D3 ID Q919D3 PRELIMINARY; PRT; 95 AA.
AC Q919D3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Neuropeptide Y.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
[1]
SEQUENCE FROM N.A.
TISSUE=BRAIN;
RA Leonard J.B.K., Waldbieser G.C., Silverstein J.T.;
RT "Neuropeptide Y (NPY) sequence and distribution in channel catfish
(ictalurus punctatus).";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE NPY / PYY / PYY FAMILY.
EMBL; AF267164; AA071617.1; -.
DR HSP; F01303; IRON.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR PRINTS; PR00278; PANCHORMONE.
DR ProDom; PD001267; Pancreatic_hormn; 1.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS00276; PANCREATIC_HORMONE_2; 1.
KW Amidation.
SQ SEQUENCE 95 AA; 10729 MW; 9AE19EAFBE24C6B5 CRC64;

Query Match 12.0%; Score 115.5; DB 13; Length 95;
Best Local Similarity 32.9%; Pred. No. 0.003;
Matches 26; Conservative 19; Mismatches 25; Indels 9; Gaps 2;

Qy 4 ARLCVLSLLSTCVALLQLLQAGAPLEVPYGDNATPEQMAQYAADLRRYINML 60
Db 5 ANVCVGAACILLVCLV-----AGYPTKPENPGEDAPVEELAKYYSALRHVINLI 58
Qy 61 TRPRCVFOLGREIPAGTTL 79
Db 59 TRQRYGKRSNTDVLTPDLL 77

RESULT 3
Q91XDO ID Q91XDO PRELIMINARY; PRT; 98 AA.
AC Q91XDO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:19143).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
TISSUE=COLON;
RA Stryausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010821; AAH10821.1; -.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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DR ProDom; PD001267; Pancreatic_hormn; 1.
PROSITE; PS00265; PANCREATIC_HORMONE_1.
DR PROSITE; PS00276; PANCREATIC_HORMONE_2; 1.
SQ SEQUENCE 98 AA; 11064 MW; 7AF165A1052C3249 CRC64;

Query Match 11.8%; Score 113.5; DB 11; Length 98;
Best Local Similarity 37.3%; Pred. No. 0.0047;
Matches 25; Conservative 16; Mismatches 15; Indels 11; Gaps 3;

Qy 10 LLLSTCVALLQLLQAGAPLEVPYGDNATPEQMAQYAADLRRYINMLTRRCVPQL 69
Db 15 LLILLACLGALV-----DAYPAKPEAPGEDASPELSRYYSALRHVLTQR-----Y 64
Qy 70 G-REIPA 75
Db 65 GKRDVPA 71

RESULT 4
O68872 ID O68872 PRELIMINARY; PRT; 542 AA.
AC O68872;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 57.2 kDa protein.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC Myxococcales; Cytophasterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
[1]
SEQUENCE FROM N.A.
RC STRAIN=DK 101;
RX MEDLINE=99047594; PubMed=9829957;
RA Harris B.Z., Singer M.;
RT "Identification and characterization of the Myxococcus xanthus arge
RT gene.";
RL J. Bacteriol. 180:6412-6414 (1998).
DR EMBL; AF055904; AAC82365.1; -.
KW Hypothetical protein.
SQ SEQUENCE 542 AA; 57203 MW; DA7E39075A86A8BC CRC64;

Query Match 11.5%; Score 111; DB 2; Length 542;
Best Local Similarity 28.6%; Pred. No. 0.053;
Matches 54; Conservative 5; Mismatches 58; Indels 72; Gaps 12;

Qy 26 GAQGAPLEVPYGDNATPEQMAQY-----ADLRRY---INMLTRRCVPQLGREIPAP 76
Db 33 GARPPPTETASYPPPPQAVPGFCAPRAPRPPPPRRRRHRSRHSFRPTCARRSGRCAP 92
Qy 77 -----GTLGPLH-----IPGHTLSPAPAP-----APSRPALGKTHLCST-GLDQC 116
Db 93 SRHARNPAGSRRCGPPRKSPTTRCTCTCPAPPRCARPSAPA-PSAGRTCTTAGPSSC 151
Qy 117 ALGKMWPTGRYETGLAPG---HSA-----
Db 152 ASG-CCPTGRC---GSAFGPTPHGAEPSPSQSPAPASSGGRRTTHPRPARASAAGAT 207
Qy 139 CPCCLFPFR 147
Db 208 APACLPPPR 216

RESULT 5
Q925V2 ID Q925V2 PRELIMINARY; PRT; 89 AA.
AC Q925V2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neuropeptide Y (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SM/J;
RX MEDLINE=21077529; PubMed=11210195;
RA Taylor B.A., Wnek C., Schroeder D., Phillips S.J.;
RT "Multiple obesity QTLs identified in an intercross between the NZO
RL (New Zealand obese) and the SM (small) mouse strains.";
RL Mamm. Genome 12:95-103(2001).
DR EMBL; AF286198; AAG01330.1; -.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR ProDom; PD001267; Pancreatic_hormn; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; UNKNOWN_1.
DR PROSITE; PS0276; PANCREATIC_HORMONE_2; 1.
FT NON TER 89
SQ SEQUENCE 89 AA; 9943 MW; AE6052615A59D96A CRC64;

Query Match 11.5%; Score 110.5; DB 11; Length 89;
Best Local Similarity 42.2%; Pred. No. 0.0079;
Matches 27; Conservative 11; Mismatches 19; Indels 7; Gaps 2;

Oy 1 MAARLCISLLSTCVALLQPLGAGAPLEVPYPCDNATPEQMAQYAADLRRYINML 60
Db 7 MGCLGLTALSLL-VCLGIL-----AGYPSKPDNPGEDAPREDMARYSALRHVYINLI 59

Oy 61 TRPR 64
Db 60 TRQR 63

RESULT 6
O90WF4 PRELIMINARY; PRT; 99 AA.
AC O90WF4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neuropeptide Y.
GN NPY.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=BRAIN;
RA Kurokawa T., Suzuki T.;
RT "Development of neuropeptide Y related peptides in the digestive
RL organs during the larval stage of Japanese flounder, Paralicthys
RL olivaceus.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB055211; BAB62409.1; -.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR ProDom; PD001267; Pancreatic_hormn; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; UNKNOWN_1.
DR PROSITE; PS0276; PANCREATIC_HORMONE_2; 1.
SQ SEQUENCE 99 AA; 11215 MW; 6FEED47F24CF6498 CRC64;

Query Match 11.5%; Score 110.5; DB 13; Length 99;
Best Local Similarity 39.3%; Pred. No. 0.0089;
Matches 24; Conservative 10; Mismatches 12; Indels 15; Gaps 1;

Oy 4 ARCLCSLLSTCVALLQPLGAGAPLEVPYPCDNATPEQMAQYAADLRRYINMLTRP 63
Db 18 ALLCLLSAL-----TEGYVPKPNPGDPAEELAKYYSALRHVYINLIITRQ 62

Oy 64 R 64
```

```
Db 63 R 63

RESULT 7
Q8SPF7 PRELIMINARY; PRT; 97 AA.
AC Q8SPF7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Neuropeptide Y precursor.
GN NPY.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ILE DE FRANCE; TISSUE=HYPOTHALAMUS;
RA Pillon D., Bruneau G.;
RT "Nucleotide sequence of Ovine preneuropeptide Y.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ417904; CAD10677.1; -.
KW Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 64 NEUROPEPTIDE Y.
FT CHAIN 68 97 POTENTIAL.
SQ SEQUENCE 97 AA; 10750 MW; 6C2209A361CF8583 CRC64;

Query Match 11.0%; Score 106; DB 6; Length 97;
Best Local Similarity 40.6%; Pred. No. 0.022;
Matches 26; Conservative 13; Mismatches 23; Indels 2; Gaps 1;

Oy 1 MAARLCISLLSTCVALLQPLGAGAPLEVPYPCDNATPEQMAQYAADLRRYINML 60
Db 2 LGSKRLGLSGLTALSLLVCLGAL--AEAYPSKPDNPGDPAEDLARYYSALRHVYINLI 59

Oy 61 TRPR 64
Db 60 TRQR 63

RESULT 8
Q9XSW6 PRELIMINARY; PRT; 97 AA.
AC Q9XSW6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Neuropeptide Y.
GN NPY.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Adler L.A., Golos T.G., Terasawa E.;
RT "Developmental changes in NPY mRNA expression in female rhesus
RL monkeys.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
DR EMBL; AF162280; AAD43583.1; -.
DR HSPF; PF1303; IRON.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR ProDom; PD00278; PANCHORMONE.
DR PROSITE; PD001267; Pancreatic_hormn; 1.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS0276; PANCREATIC_HORMONE_2; 1.
```

QW	Amidation.	97 AA	10840 MW	2D2209BAC20BD5EE CRC64	
QW	SEQUENCE	97 AA	10840 MW	2D2209BAC20BD5EE CRC64	1
QW	Query Match	10.9%	Score 105;	DB 6;	Length 97;
QW	Best Local Similarity	40.6%	Pred. No. 0.027;		
QW	Matches	26;	Conservative	13;	Mismatches 23; Indels 2; Gaps 1;
QY	1	MAAARCLCLLLSTCTCVALLLOPLLGAGCAPLEVPYVPGDNATPEQMAQYAADLRRYINML	60		
Db	2	LGSKRGLSGLTLALSLLVCLGAL--AEAYPSKDPNFGDAPADMDARYYSALRHYINLI	59		
QY	61	TRPR	64		
Db	60	TRQR	63		
RESULT	9				
Q90WF3	PRELIMINARY;	PRT;	99 AA.		
AC	Q90WF3;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE	Peptide YY.				
GN	PYY.				
OS	Paralichthys olivaceus (Flounder).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;				
OC	Pleuronectoidae; Paralichthyidae; Paralichthys.				
NCBI	NCBI_TaxID=8255;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BRAIN;				
RA	Kurokawa T.; Suzuki T.;				
RA	"Development of neuropeptide Y related peptides in the digestive				
RT	organs during the larval stage of Japanese flounder, Paralichthys				
RT	olivaceus."				
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB055212; BAB62410.1; "				
DR	InterPro; IPR001955; Pancreatic_hormn.				
DR	Pfam; PF00159; hormone3; 1;				
DR	ProDom; PD001267; Pancreatic_hormn; 1.				
DR	PROSITE; PS00265; PANCREATIC_HORMONE_1; UNKNOWN_1.				
DR	PROSITE; PS0276; PANCREATIC_HORMONE_2; 1.				
QW	SEQUENCE	99 AA;	11179 MW;	32F6C21217CB1984 CRC64;	
QY	Query Match	10.9%;	Score 105;	DB 13;	Length 99;
QY	Best Local Similarity	34.4%;	Pred. No. 0.028;		
QY	Matches	22;	Conservative	14;	Mismatches 26; Indels 2; Gaps 1;
QY	1	MAAARCLCLLLSTCTCVALLLOPLLGAGCAPLEVPYVPGDNATPEQMAQYAADLRRYINML	60		
Db	1	MIRSTWSPSVLALCLLACIHS--GINAYPVKPTIPREGATPEDLAKYYSALRHYINLI	58		
QY	61	TRPR	64		
Db	59	TRQR	62		
RESULT	10				
Q9TS16	PRELIMINARY;	PRT;	90 AA.		
AC	Q9TS16;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	Neuropeptide Y (Fragment).				
OS	Ovis aries (Sheep).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Caprinae; Ovis.				
NCBI	NCBI_TaxID=9940;				

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FT PEPTIDE 29 64 NEUROPEPTIDE Y.
FT PROPEP 68 97 BY SIMILARITY.
FT MOD_RES 64 64 AMIDATION (G-65 PROVIDE AMIDE GROUP)
FT SEQUENCE 97 AA; 11275 MW; 96829D9DFFB1C7 CRC64;

Query Match 10.8%; Score 104; DB 13; Length 97;
Best Local Similarity 41.7%; Pred. No. 0.034;
Matches 25; Conservative 11; Mismatches 22; Indels 2; Gaps 1;

QY 5 RUCSLILLSTCVALLLOPLGACQALEPVVYVGNATPEQMAQYAADLRVYINMLTRPR 64
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 6 RLWLSVLFTLSLLICLGTLL--ADAYPSKPNPGEDAPADMAYISALRYHINILTRQR 63

RESULT 12
O52861 PRELIMINARY; PRT; 387 AA.
AC O52861;
OS 01-JUN-1998 (TRENBLrel. 06, Created)
OC 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE YrBA protein.
GN YrBA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=60015;
RX MEDLINE=98442430; PubMed=9770294;
RA Takamatsu H., Hiraoka T., Kodama T., Koide H., Kozuka S.,
RA Tochikubo K., Watabe K.;
RT "Cloning of a novel gene yrbB, encoding a protein located in the spore
RT integument of Bacillus subtilis.";
RL FEMS Microbiol. Lett. 166:361-367(1998).
DR EMBL; D50551; BAA24943.1; -.
DR InterPro; IPR002482; LysM.
DR Pfam; PF01476; LysM; 1.
DR SMART; SM00257; LysM; 1.
DR SEQUENCE 387 AA; 43213 MW; F050ABF6F185DBFC CRC64;

Query Match 10.6%; Score 102.5; DB 2; Length 387;
Best Local Similarity 25.5%; Pred. No. 0.21;
Matches 40; Conservative 21; Mismatches 69; Indels 27; Gaps 7;

32 LEPVYVGNATPEQMAQYAADLRVYINMLTRPCVPLG-----REIPAGTLG 80
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 145 MDHYMHMQDQFPQQAEMSNMENANYPNNMPK-APEYGVGEENVHHTVPMMPAVQP 203

QY 81 PLHIGHTLSAPAPASRPALGKTHLCSTGLDQCALGKMVPTGRYETGGLAPGHSACP 140
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 204 YVYHAFV---PCVPVSPILPGSG-ICYPYPAQAF-PNHPMHGYQPGVSP----- 252

QY 141 CCLFPYRKGKHKEDTL--AFSEWGSPhAAVPRELSP 175
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 253 --QYDPGVENQHENTHGHVGSYGAPQVAPYAGSP 287

RESULT 13
Q9RKR9 PRELIMINARY; PRT; 1334 AA.
AC Q9RKR9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE Putative multi-domain regulatory protein.
GN SC02259 OR SC075A.05C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL13220; CAB61705.1; -.
DR InterPro; IPR005158; BAD.
DR InterPro; IPR000767; Disease_resist.
DR Pfam; PF03704; BAD; 1.
DR PRINTS; PR00364; DISEASERSIST.
DR PRINTS; PR01574; TUBBYPROTEIN.
DR ProDom; PD000329; Trans_reg_C; 1.
DR SEQUENCE 1334 AA; 138787 MW; 78DC746883E8778C CRC64;

Query Match 10.6%; Score 102; DB 16; Length 1334;
Best Local Similarity 30.8%; Pred. No. 0.93;
Matches 36; Conservative 6; Mismatches 63; Indels 12; Gaps 4;

QY 31 LPEVYVGNATPEQMAQYAADLRVYINMLTRPCVPLGREIPAGTLGLPHIGHTLS 90
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 319 PAPGTAPGSTAPPHTASADTAPAPGPTSAPGTAPAAAGTAAPAGTAGP--APGTSYA 376

QY 91 PAPA-----PAP-SRPALGKTHLCSTGLDQCALGKMVPTGRYETGGLAPGHSACP 140
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 377 PGTAPVAGTTPAGTAPAGTAPGTPARDTSY---APGTAPVAGTTPAGTAPAGSTP 430

RESULT 14
Q9NYQ6 PRELIMINARY; PRT; 3014 AA.
AC Q9NYQ6; O95722; Q9Y526;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Protocadherin Flamingo 2 (Dj1163J1.1) (Dj439F8.2).
GN FM12 OR Dj1163J1.1 OR Dj439F8.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99308636; PubMed=10380929;
```

RA Wu Q., Maniatis T.;  
RT "A striking organization of a large family of human neural cadherin-  
RL like cell adhesion genes.";  
RN Cell 97:779-790(1999).  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20202599; PubMed=10716726;  
RA Wu Q., Maniatis T.;  
RT "Large exons encoding multiple ectodomains are a characteristic  
RT feature of protocadherin genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).  
RN [3]  
RP SEQUENCE OF 1-1181 FROM N.A.  
RA Williams S.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 1538-3014 FROM N.A.  
RA Lloyd D.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.  
EMBL; AF231024; AAF61930.1; -;  
EMBL; AL021392; CAB50707.1; -;  
EMBL; AL031588; CAB38413.1; -;  
DR HSSP; P00749; IURC.  
DR HSSP; P15116; INCU.  
DR InterPro; IPR000152; Asx hydroxyl.  
DR InterPro; IPR002126; Cadherin.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR000832; GPCR\_secretin.  
DR InterPro; IPR001879; hormn\_receptor.  
DR InterPro; IPR002049; Laminin\_EGF.  
DR InterPro; IPR001791; Laminin\_G.  
DR InterPro; IPR000203; PKD\_cys\_rich.  
DR Pfam; PF00002; 7tm 2; 1\_1\_cys\_rich.  
DR Pfam; PF00028; cadherin; 8.  
DR Pfam; PF00008; EGF; 6.  
DR Pfam; PF01825; GPS; 1.  
DR Pfam; PF02793; HRM; 1.  
DR Pfam; PF00053; laminin\_EGF; 1.  
DR Pfam; PF00054; laminin\_G; 1.  
DR PRINTS; PR00205; CADHERIN.  
DR PRINTS; PR00011; EGF\_LAMININ.  
DR PRINTS; PR00249; GPCR\_SECRETIN.  
DR SMART; SM00112; CA; 9.  
DR SMART; SM00180; EGF\_Lam; 1.  
DR SMART; SM00001; EGF\_like; 6.  
DR SMART; SM00303; GPS; 1.  
DR SMART; SM00008; Hormr; 1.  
DR SMART; SM00282; LamG; 2.  
DR PROSITE; PS00010; ASX HYDROXYL; UNKNOWN\_2.  
DR PROSITE; PS00232; CADHERIN\_1; 6.  
DR PROSITE; PS02368; CADHERIN\_2; 9.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_6.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS00227; G-PROTEIN RECEPTOR\_2; 3; 1.  
DR PROSITE; PS00261; G-PROTEIN RECEPTOR\_2; 4; 1.  
DR PROSITE; PS01248; LAMININ TYPE EGF; UNKNOWN\_1.  
KW Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein.  
SQ SEQUENCE 3014 AA; 329481 MW; C34691AD3A1DFF3A CRC64;  
  
Query Match 10.6%; Score 102; DB 4; Length 3014;  
Best Local Similarity 29.3%; Pred. No. 2.3;  
Matches 49; Conservative 9; Mismatches 63; Indels 46; Gaps 8;  
  
QY 10 LLLSTCVALLQLLOPLGAGAPLEPVYPGDNATPEQMAQYAADLRRYINMLTRPCVPOL 69  
Db LLLLAALAAAL---PAMGLRAAWEPVPGTR-----AFALRPGCTYAVGALCTPRA 60  
QY 70 GREIPAPGTILG-----PLHIFGHTLSAPAPAPSR-----PALGKTGHL 108  
Db PRELLDVGDRGLAGRRRVSGAGRPPLQVRLVARSAPTALSRRLRARTLPGCCGARARL 120  
QY 109 CST&LDQC-ALGKMTPTGRTYETGGLAPG-HSA-----CPCCLFPFR 147

Db 121 CGTGARLGCALGCFPPV-----GGCAAQHSAALAAPTTLPAACRCPPR 161  
RESULT 15  
Q9DGK7 PRELIMINARY; PRT; 96 AA.  
AC Q9DGK7;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE Neuropeptide Y.  
OS Cyprinus carpio (Common carp).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Cyprinus.  
OX NCBI\_TaxID=7962;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RA Yingwen L., Takeshi Y.;  
RT "Daily rhythmic gene expression of neuropeptide Y in discrete brain of  
RT common carp, Cyprinus carpio, under the condition of self feeding.";  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.  
DR EMBL; AF287347; AAG00549.1; -;  
DR HSSP; P01303; IRON.  
DR InterPro; IPR001955; Pancreat\_hormn.  
DR Pfam; PF00159; hormone3; 1.  
DR PRINTS; PR00278; PANCHORMONE.  
DR ProDom; PD001267; Pancreat\_hormn; 1.  
DR SMART; SM00309; PAH; 1.  
DR PROSITE; PS00265; PANCREATIC\_HORMONE\_1; 1.  
DR PROSITE; PS00276; PANCREATIC\_HORMONE\_2; 1.  
KW Amidation.  
SQ SEQUENCE 96 AA; 10987 MW; C6C5ABCD87688980 CRC64;  
  
Query Match 10.5%; Score 101; DB 13; Length 96;  
Best Local Similarity 44.9%; Pred. No. 0.062;  
Matches 22; Conservative 10; Mismatches 15; Indels 2; Gaps 1;  
  
QY 18 ALLQLPLG--AAGAPLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64  
Db AFLFLACLGLTLEGYPTKPNPGEDAPAEELAKYYSALRHYINLITRQR 63  
  
Search completed: March 1, 2003, 09:13:21  
Job time : 34 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:11:12 ; Search time 17 Seconds  
(without alignments)  
1006.584 Million cell updates/sec

Title: US-09-965-528-16  
Perfect score: 964  
Sequence: 1 MAARLCISLLSLTCTVALL.....FSEWGSPHAAVPRELSPLDL 178

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Search: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 73:.\*  
1: Pirl.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	441.5	45.8	95	1 PCHU	pancreatic hormone
2	305.5	31.7	93	1 PCDG	pancreatic hormone
3	260.5	27.0	100	2 B28261	pancreatic hormone
4	249.5	25.9	66	1 PCCT	pancreatic hormone
5	244.5	25.4	126	2 A28236	pancreatic hormone
6	236.5	24.5	98	1 PCRT	pancreatic hormone
7	207.5	21.5	59	1 PCST	pancreatic hormone
8	186	19.3	36	2 C60071	pancreatic hormone
9	182	18.9	36	1 C61132	pancreatic hormone
10	180	18.7	36	1 A61132	pancreatic hormone
11	180	18.7	36	1 D61132	pancreatic hormone
12	180	18.7	36	2 B60413	pancreatic hormone
13	177	18.4	36	1 PCFG	pancreatic hormone
14	176	18.3	36	1 PCBO	pancreatic hormone
15	172	17.8	36	1 B61132	pancreatic hormone
16	161	16.7	36	2 J00365	pancreatic hormone
17	140	14.5	93	2 I50809	peptide YY - river
18	123	12.8	36	2 A28091	pancreatic hormone
19	116	12.0	98	2 A29364	peptide YY precurs
20	114	11.8	36	1 PCFG	pancreatic hormone
21	111.5	11.6	98	2 A25916	neuropeptide Y pre
22	110.5	11.5	97	2 JCL140	neuropeptide Y pre
23	110	11.4	80	1 PCCH	pancreatic hormone
24	109	11.3	90	2 S34569	peptide YY precurs
25	109	11.3	90	2 S34568	peptide YY precurs
26	109	11.3	97	2 S33795	peptide YY (clone
27	106	11.0	36	1 PCAQ	pancreatic hormone
28	103.5	10.7	97	1 NYTHUY	neuropeptide Y pre
29	103	10.7	97	2 A41979	neuropeptide Y pre

RESULT 1  
PCHU

Pancreatic hormone precursor [validated] - human  
N;Alternate names: pancreatic polypeptide precursor  
N;Contains: pancreatic heptapeptide; pancreatic icosapeptide  
C;Species: Homo sapiens (man)  
C;Date: 17-Dec-1982 #sequence revision 25-Feb-1985 #text change 08-Dec-2000  
C;Accession: A92498; A91002; A22587; I70196; A94026; A94018; A60088; A01566  
R;Leiter, A.B.; Montminy, M.R.; Jamieson, E.; Goodman, R.H.  
J. Biol. Chem. 260, 13013-13017, 1985  
A;Title: Exons of the human pancreatic polypeptide gene, define functional domains of the  
A;Reference number: A92498; MUID:86033734; PMID:2997153  
A;Accession: A92498  
A;Molecule type: DNA  
A;Residues: 1-95 <LEI1>  
A;Cross-references: GB:M11726; NID:g190269; PIDN:AAA60156.1; PID:g190270  
R;Boel, E.; Schwartz, T.W.; Norris, K.E.; Fill, N.P.  
EMBO J. 3, 909-912, 1984  
A;Title: A cDNA encoding a small common precursor for human pancreatic polypeptide and  
A;Reference number: A91002; MUID:84207951; PMID:6373251  
A;Accession: A91002  
A;Molecule type: mRNA  
A;Residues: 1-95 <BOE>  
A;Cross-references: GB:X00491; NID:g35589; PIDN:CAA25161.1; PID:g35590  
R;Leiter, A.B.; Keutmann, H.T.; Goodman, R.H.  
J. Biol. Chem. 259, 14702-14705, 1984  
A;Title: Structure of a precursor to human pancreatic polypeptide.  
A;Reference number: A22587; MUID:85054955; PMID:6094571  
A;Accession: A22587  
A;Molecule type: mRNA  
A;Residues: 1-95 <LEI2>  
A;Note: Part of this sequence, including the amino end of the mature protein, was deter  
R;Takeuchi, T.; Gumucio, D.L.; Yamada, T.; Meisler, M.H.; Minth, C.D.; Dixon, J.E.; Edd  
J. Clin. Invest. 77, 1038-1041, 1986  
A;Title: Genes encoding pancreatic polypeptide and neuropeptide Y are on human chromos  
A;Reference number: I55543; MUID:86140715; PMID:3753985  
A;Accession: I70196  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-85, 'I', 87-95 <TAK1>  
A;Cross-references: GB:M15788; NID:g190301; PIDN:AAA60161.1; PID:g190302  
R;Takeuchi, T.; Yamada, T.  
Proc. Natl. Acad. Sci. U.S.A. 82, 1536-1539, 1985  
A;Title: Isolation of a cDNA clone encoding pancreatic polypeptide.  
A;Reference number: A94026; MUID:85140331; PMID:3856278  
A;Accession: A94026  
A;Molecule type: mRNA  
A;Residues: 1-85, 'I', 87-95 <TAK2>  
R;Schwartz, T.W.; Hansen, H.F.; Hakanson, R.; Sundler, F.; Tager, H.S.  
Proc. Natl. Acad. Sci. U.S.A. 81, 708-712, 1984  
A;Title: Human pancreatic icosapeptide: isolation, sequence, and immunocytochemical loca  
A;Reference number: A94018; MUID:84144773; PMID:6366786

ALIGNMENTS

30	102	10.6	104	2	I50808	neuropeptide Y pre
31	102	10.6	1334	2	T50568	probable multi-dom
32	101	10.5	37	2	S26954	peptide YY-related
33	100	10.4	96	2	B41979	neuropeptide Y pre
34	99	10.3	36	1	YYFG	peptide YY - pig
35	99	10.3	36	2	A31358	peptide YY - human
36	99	10.3	36	2	A60416	peptide YY - dog
37	98.5	10.2	2205	1	MNWMVN	nonstructural poly
38	98	10.2	97	2	A55914	peptide YY precurs
39	97.5	10.1	387	2	H69971	spore coat protein
40	97.5	10.1	1042	1	CGGH1S	collagen alpha 1(I
41	97	10.1	1373	1	A43291	collagen alpha 2(I
42	96	10.0	36	1	PCGXA	pancreatic peptide
43	96	10.0	36	1	PCDFY	pancreatic peptide
44	96	10.0	36	2	A49743	pancreatic peptide
45	95.5	9.9	2115	2	S38480	nonstructural prot

A;Accession: A94018  
A;Molecule type: protein  
A;Residues: 69-88 <SCH>  
R;Gingerich, R.L.; Akpan, J.O.; Leith, K.M.; Gilbert, W.R.  
Regul. Pept. 33, 275-285, 1991  
A;Title: Patterns of immunoreactive pancreatic polypeptide in human plasma.  
A;Reference number: A60068; MUID:91352354; PMID:1882090  
A;Accession: A60068  
A;Molecule type: protein  
A;Residues: 32-47 <GIN>  
C;Genetics:  
A;Gene: GDB:PPY  
A;Cross-references: GDB:120311; OMIM:167780  
A;Map position: 17q12-17q21  
A;Introns: 64/2: 88/2  
C;Superfamily: pancreatic hormone  
C;Keywords: amidated carboxyl end; hormone; pancreas  
F;1-29/Domain: signal sequence #status predicted <Sig>  
F;30-65/Product: pancreatic hormone #status predicted <PCH>  
F;69-88/Product: pancreatic icosaapeptide #status experimental <PCI>  
F;89-95/Product: pancreatic heptaapeptide #status predicted <PC7>  
F;95/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

Query Match 45.8%; Score 441.5; DB 1; Length 95;  
Best Local Similarity 53.4%; Pred. No. 7e-28;  
Matches 95; Conservative 0; Mismatches 0; Indels 83; Gaps 1;  
Qy 1 MAAARCLSLLLSTCVALLQLPLGAGAPLEPVPGDNATPEQMAQYAADLRRYINML 60  
Db 1 MAAARCLSLLLSTCVALLQLPLGAGAPLEPVPGDNATPEQMAQYAADLRRYINML 60  
Qy 61 TRPRCVPOLGREIPAGTGLPHIPGHTLSPAPAPSRPALGKTGHLCTGLDQCALGK 120  
Db 61 TR-----PRYGRKRDGEMRDILEWGSPPHAAAPREL 90  
Qy 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPPHAAVPRELSPDL 178  
Db 63 -----PRYGRKHKEDTLAFSEWGSPPHAAVPRELSPDL 95  
RESULT 2  
PCDG  
pancreatic hormone precursor - dog  
N;Alternate names: pancreatic polypeptide precursor  
N;Contains: pancreatic hormone; pancreatic icosaapeptide  
C;Species: Canis lupus familiaris (dog)  
C;Date: 25-Feb-1985 #sequence\_revision 12-Apr-1996 #text\_change 18-Jun-1999  
C;Accession: A40904; A94465; A93270; A01567  
R;Toothman, P.; Paquette, T.L.  
A;Title: Canine pancreatic polypeptide complementary deoxyribonucleic acid sequence: pan  
A;Reference number: A40904; MUID:90331935; PMID:3079195  
A;Accession: A40904  
A;Molecule type: mRNA  
A;Residues: 1-93 <TOO>  
A;Cross-references: GB:M35596; NID:g164049; PIDN:AAA30886.1; PID:g164050  
A;Note: the authors translated the codon CCT for residue 2 as Ala, and GAG for residue 5  
R;Chance, R.E.; Johnson, M.G.; Hoffmann, J.A.; Jones, W.E.; Koffenberger Jr., J.E.  
unpublished results, cited by Chance, R.E., Moon, N.E., and Johnson, M.G., in Methods of  
San Francisco, and London, 1979  
A;Reference number: A94465  
A;Accession: A94465  
A;Molecule type: protein  
A;Residues: 30-65 <CHA>  
R;Schwartz, T.W.; Tager, H.S.  
Nature 294, 589-591, 1981  
A;Title: Isolation and biogenesis of a new peptide from pancreatic islets.  
A;Reference number: A93270; MUID:82080694; PMID:70311480  
A;Accession: A93270  
A;Molecule type: protein  
A;Residues: 69-88 <SCH>  
C;Comment: The hormone precursor molecules are stored in islet cells of the duodenal pan  
C;Superfamily: pancreatic hormone

C;Keywords: amidated carboxyl end; hormone; pancreas  
F;1-20/Domain: signal sequence #status predicted <Sig>  
F;30-65/Product: pancreatic hormone #status experimental <PCH>  
F;69-88/Product: pancreatic icosaapeptide #status experimental <PCI>  
F;65/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

Query Match 31.7%; Score 305.5; DB 1; Length 93;  
Best Local Similarity 40.5%; Pred. No. 2.8e-17;  
Matches 70; Conservative 5; Mismatches 15; Indels 83; Gaps 1;  
Qy 1 MAAARCLSLLLSTCVALLQLPLGAGAPLEPVPGDNATPEQMAQYAADLRRYINML 60  
Db 1 MPAACRCLFLLLSACVALLQLPLGTRGAPLEPVPGDDATPEQMAQYAALRRYINML 60  
Qy 61 TRPRCVPOLGREIPAGTGLPHIPGHTLSPAPAPSRPALGKTGHLCTGLDQCALGK 120  
Db 61 TR-----PRYGRKRDGEMRDILEWGSPPHAAAPREL 90  
Qy 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPPHAAVPREL 173  
Db 63 -----PRYGRKRDGEMRDILEWGSPPHAAAPREL 90  
RESULT 3  
B28261  
pancreatic hormone precursor - mouse  
N;Alternate names: pancreatic polypeptide precursor  
N;Contains: pancreatic hormone; pancreatic icosaapeptide  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 16-Jul-1999  
C;Accession: B28261  
R;Yonekura, H.; Nata, K.; Watanabe, T.; Kurashina, Y.; Yamamoto, H.; Okamoto, H.  
J. Biol. Chem. 263, 2990-2997, 1988  
A;Title: Mosaic evolution of prepropancreatic polypeptide. Structural conservation and  
A;Reference number: A92708; MUID:88139354; PMID:3343236  
A;Accession: B28261  
A;Molecule type: DNA  
A;Residues: 1-100 <YON>  
A;Cross-references: GB:M18208; GB:J03543; NID:g200463; PIDN:AAA39967.1; PID:g200464  
C;Superfamily: pancreatic hormone  
C;Keywords: amidated carboxyl end; hormone; pancreas  
F;1-29/Domain: signal sequence #status predicted <Sig>  
F;30-65/Product: pancreatic hormone #status predicted <PCH>  
F;71-100/Product: pancreatic icosaapeptide #status predicted <PCI>  
F;65/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

Query Match 27.0%; Score 260.5; DB 2; Length 100;  
Best Local Similarity 61.1%; Pred. No. 9.7e-14;  
Matches 58; Conservative 5; Mismatches 25; Indels 7; Gaps 2;  
Qy 1 MAAARCLSLLLSTCVALLQLPLGAGAPLEPVPGDNATPEQMAQYAADLRRYINML 60  
Db 1 MAVAYCCLSLFLVSTWALLQLPLQGTWAPLEPMYPGDYATPEQMAQYETQLRRYINML 60  
Qy 61 TRPRCVPOLGREIPAGTGLPHIPGHTLSPAPAP 95  
Db 61 TRPR-----YGRABEENTGG---LPGVQLSPECTSP 88  
RESULT 4  
PCTT  
pancreatic hormone precursor - cat (tentative sequence) (fragment)  
N;Alternate names: pancreatic polypeptide precursor  
N;Contains: pancreatic hormone; pancreatic icosaapeptide  
C;Species: Felis silvestris catus (domestic cat)  
C;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1988 #text\_change 31-Mar-2000  
C;Accession: A26073  
R;Nielsen, H.V.; Gether, U.; Schwartz, T.W.  
Biochem. J. 240, 69-74, 1986  
A;Title: Cat pancreatic eicosapeptide and its biosynthetic intermediate. Conservation c  
A;Reference number: A26073; MUID:87156600; PMID:3827854  
A;Accession: A26073  
A;Molecule type: protein

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A;Residues: 1-66 <NTB>
C;Comment: We have added, by homology with the human precursor sequence, Gly-37, which is
C;Superfamily: pancreatic hormone
C;Keywords: amidated carboxyl end; hormone; pancreas
F;1-36/Product: pancreatic hormone #status experimental <PCH>
F;40-66/Product: pancreatic icosa-peptide #status experimental <PCI>
F;36/Modified site: amidated carboxyl end (1yr) (amide in mature form from following gly

Query Match          25.9%   Score 249.5; DB 1; Length 66;
Best Local Similarity 36.9%; Pred. No. 4.7e-13;
Matches 55; Conservative                    5; Mismatches 6; Indels 83; Gaps 1;

QY 30 APLEVPVPGDNATPEQMAQYAADLRRYNNLMTRPRCPVQLGRETPAPGTLGLPHIPGHHTL 89
Db 1 APLEVPVPGDNATPEQMAQYAADLRRYNNLMTR----- 33

QY 90 SPAPAPSRPALCKTGHLCSTGLDQCALGWVPTGRYETGGLAPGHSACPCCLFPPTYG 149
34 -----PRYG 37

150 KRHKEDTLAFSEMGSPHAAVPRELSPLDL 178
|| : ||| ||||| ||| | ||| :| :| :| :|
Db 38 KRDRETLDILEWGSFHAAAPRELSPMDV 66

RESULT 5
A28256
pancreatic hormone precursor - guinea pig
N;Alternate names: pancreatic polypeptide precursor
N;Contains: pancreatic hormone; pancreatic icosa-peptide
C;Species: Cavia porcellus (guinea pig)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: A28256
R;Blackstone, C.D.; Seino, S.; Takeuchi, T.; Yamada, T.; Steiner, D.F.
J. Biol. Chem. 263, 2911-2916, 1988
A;Title: Novel organization and processing of the guinea pig pancreatic polypeptide precur
A;Reference number: A28256; PMID:88139344; PMID:2830269
A;Accession: A28256
A;Molecule type: mRNA
A;Residues: 1-126 <BLA>
A;Cross-references: GB:M29543; NID:g191292; PIDN:AAA37051.1; PID:g305340; GB:J03532
C;Superfamily: pancreatic hormone
C;Keywords: amidated carboxyl end; hormone; pancreas
F;1-26/Dominant signal sequence #status predicted <SIG>
F;27-62/Product: pancreatic hormone #status predicted <PCH>
F;67-126/Product: pancreatic icosa-peptide #status predicted <PCI>
F;62/Modified site: amidated carboxyl end (1yr) (amide in mature form from following gly

Query Match          25.4%   Score 244.5; DB 2; Length 126;
Best Local Similarity 52.7%; Pred. No. 2.1e-12;
Matches 59; Conservative                    9; Mismatches 29; Indels 15; Gaps 4;

QY 1 MAARLCISLLILSTCVALLLPILLGAQGPLEVPVPGDNATPEQMAQYAADLRRYNNML 60
Db 1 MTATRCCLWLILLTGTCMALIPE---AWGAPLEVPVPGDDATPQQAQYAEMRRYYNNML 57

QY 61 TRPRCPVLGREIPAPCTLGPHLPCHLTSPA-----PAPASRPALCKGTG 106
Db 58 TRPR----YKSAEEDALGUPVWRQSHAAAPGGSHRHPAGLPFA--AKGTG 103

RESULT 6
PCRT
pancreatic hormone precursor - rat
N;Alternate names: pancreatic polypeptide precursor
N;Contains: pancreatic hormone; pancreatic icosa-peptide
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999
C;Accession: A28261; S06472; J01571
R;Yonekura, H.; Nata, K.; Watanabe, T.; Kurashina, Y.; Yamamoto, H.; Okamoto, H.
J. Biol. Chem. 263, 2990-2997, 1988
A;Title: Mosaic evolution of prepropancreatic polypeptide. Structural conservation and d
A;Reference number: A92708; PMID:88139354; PMID:3343216

```

A:Accession: A28261  
A:Molecule type: DNA  
A:Residues: 1-98 <YON>  
A:Cross-references: GB:M18207; GB:J03543; NID:g206325; PIDN:AAA41922.1; PID:g206326  
R:Kopin, A.S.; Toder, A.E.; Leiter, A.B  
Arch. Biochem. Biophys. 267, 742-748, 1988  
A:Title: Different splice site utilization generates diversity between the rat and human  
A:Reference number: S06472; MUID:89104395; PMID:3214179  
A:Accession: S06472  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-98 <KOP>  
A:Cross-references: GB:M27450; NID:g341701; PIDN:AAA99236.1; PID:g602487.  
R:Yamamoto, H.; Nata, K.; Okamoto, H.  
J. Biol. Chem. 261, 6156-6159, 1986  
A:Title: Mosaic evolution of prepropancreatic polypeptide.  
A:Reference number: A01571; MUID:86196026; PMID:3009446  
A:Accession: A01571  
A:Molecule type: mRNA  
A:Residues: 1-98 <YAM>  
A:Cross-references: GB:M13588; NID:g206327; PIDN:AAA41923.1; PID:g206328  
C:Genetics:  
A:Introns: 64/2  
C:Superfamily: pancreatic hormone  
C:Keywords: amidated carboxyl end; hormone; pancreas  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-65/Product: pancreatic hormone #status predicted <PCH>  
F:69-98/Product: pancreatic icosa-peptide #status predicted <PCI>  
F:65/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly)

Query Match 24.5%; Score 236.5; DB 1; Length 98;  
Best Local Similarity 49.6%; Pred. No. 7.1e-12;  
Matches 61; Conservative 6; Mismatches 27; Indels 29; Gaps 5;

Qy 1 MAARLCISLLLSLTCVALLQPLGAGAPLEPVPDGNATPEQMAQYAADLRRYINML 60  
Db 1 MAVAYCYCLSLFLSLTVALLLQPLQGAWGAPLEPMPYEGDYATHEQRAQYETQLRRYINTL 60

Qy 61 TRPRCVQLGRIEIPAPGTGLPLHPHGTLSAPAPAPSRPALGKTHGLCST--GLDQCA 117  
Db 61 TRPR-----YQKR--DEDTAG---LPGQLPP-----CTSLLVGLMPCA 94

Qy 118 LGK 120  
Db 95 AAR 97

RESULT 7  
PCSH  
pancreatic hormone precursor - sheep (tentative sequence) (fragment)  
N:Alternate names: pancreatic polypeptide precursor  
N:Contains: pancreatic hormone; pancreatic icosa-peptide  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 25-Feb-1985 #sequence revision 25-Feb-1985 #text\_change 31-Mar-2000  
C:Accession: B94465; A91323; A01569  
R:Chance, R.E.; Johnson, M.G.; Hoffmann, J.A.; Jones, W.E.; Koffenberger Jr., J.E.  
unpublished results, cited by Chance, R.E., Moon, N.E., and Johnson, M.G., in Methods of  
San Francisco, and London, 1979  
A:Reference number: A94465  
A:Accession: B94465  
A:Molecule type: protein  
A:Residues: 1-36 <CHA>  
R:Schwartz, T.W.; Hansen, H.F.  
FEBS Lett. 166, 293-298, 1984  
A:Title: Isolation of ovine pancreatic icosa-peptide: a peptide product containing one cy  
A:Reference number: A91323; MUID:84208777; PMID:6723953  
A:Accession: A91323  
A:Molecule type: protein  
A:Residues: 40-59 <SCH>  
C:Comment: We have added, by homology with the human precursor sequence, Gly-37, which  
C:Superfamily: pancreatic hormone  
C:Keywords: amidated carboxyl end; hormone; pancreas  
F:1-36/Product: pancreatic hormone #status experimental <PCH>







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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:11:12 ; Search time 12 Seconds  
(without alignments)  
615.232 Million cell updates/sec

Title: US-09-965-528-16

Perfect score: 964

Sequence: 1 MAARLCLSLLLSTCVALL.....FSEWGSFHAAPRELSPLDL 178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 112892 seqs, 41476328 residues

al number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwisProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	441.5	45.8	95	1 PAHO HUMAN	P01298 homo sapien
2	349.5	36.3	131	1 PAHO BOVIN	P01302 bos taurus
3	305.5	31.7	93	1 PAHO CANFA	P01299 canis famil
4	260.5	27.0	100	1 PAHO MOUSE	P10601 mus musculus
5	249.5	25.9	66	1 PAHO FELCA	P06884 felis silve
6	244.5	25.4	126	1 PAHO CAVEO	P13083 cavia porce
7	236.5	24.5	98	1 PAHO RAT	P06303 rattus norv
8	207.5	21.5	59	1 PAHO SHEEP	P01301 ovis aries
9	186	19.3	36	1 PAHO MACMU	P33684 macaca mula
10	182	18.9	36	1 PAHO TAPPI	P39859 tapirus pin
11	180	18.7	36	1 PAHO CHIBR	P41519 chinchilla
12	180	18.7	36	1 PAHO EQUZE	P38000 equus zebra
13	177	18.4	36	1 PAHO PIG	P01300 sus scrofa
14	176	18.3	36	1 PAHO CERSI	P37999 ceratotheri
15	173	17.9	36	1 PAHO ERIEU	P41335 erinaceus e
16	167	17.3	36	1 PAHO RABIT	P41336 oryctolagus
17	161	16.7	36	1 PAHO DIOMA	P18107 didelphis m
18	140	14.5	93	1 PYU LAMFL	P48098 lampetra fl
19	123	12.8	36	1 PAHO RANCA	P15427 rana catesb
20	116	12.0	98	1 PYU RAT	P10631 rattus norv
21	115.5	12.0	95	1 NEUY ICTPU	P919d3 ictalurus p
22	114	11.8	36	1 PAHO RANTE	P31229 rana tempor
23	113.5	11.8	93	1 PYU MOUSE	O9eps2 mus musculu
24	111.5	11.6	97	1 NEUY MOUSE	P57774 mus musculu
25	111.5	11.6	98	1 NEUY RAT	P07808 rattus norv
26	110.5	11.5	97	1 NEUY XENLA	P33689 xenopus lae
27	110	11.4	80	1 PAHO CHICK	P01306 gallus gall
28	109	11.3	97	1 PYU HUMAN	P10082 homo sapien
29	108	11.2	97	1 PYU BRARE	O918p2 brachydanio
30	107	11.1	97	1 PY DICLA	O9pt98 dicentrarch
31	106	11.0	36	1 PAHO ALLMI	P06305 alligator m
32	106	11.0	99	1 PYU DICLA	O9pt99 dicentrarch
33	104.5	10.8	96	1 NEUY BRARE	O918p3 brachydanio

34	103.5	10.7	97	1 NEUY HUMAN	P01303 homo sapien
35	103	10.7	97	1 NEUY CHICK	P28673 gallus gall
36	102.5	10.6	99	1 NEUY DICLA	O9pta0 dicentrarch
37	102	10.6	104	1 NEUY LAMFL	P48097 lampetra fl
38	102	10.6	3014	1 CLRI HUMAN	O9nyq6 homo sapien
39	101	10.5	36	1 PYU RAJRH	P29206 raja rhina
40	101	10.5	37	1 PYU CHICK	P29203 gallus gall
41	100	10.4	96	1 NEUY CARAU	P28672 carassius a
42	99	10.3	36	1 PYU FIG	P13305 sus scrofa
43	98.5	10.2	2205	1 POLN RUBVT	P13889 rubella vir
44	98	10.2	97	1 PYU BOVIN	P51694 bos taurus
45	97.5	10.1	1453	1 CALI CHICK	P02457 gallus gall

## ALIGNMENTS

RESULT 1  
PAHO HUMAN  
ID PAHO HUMAN STANDARD; PRT; 95 AA.  
AC P01298;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pancreatic hormone precursor (Pancreatic polypeptide) (PP).  
GN PPY OR PNP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84207951; PubMed=6373251;  
RA Boel E., Schwartz T.W., Norris K.E., Fiil N.P.;  
RT "A cDNA encoding a small common precursor for human pancreatic  
polypeptide and pancreatic icosapeptide.";  
RL EMBO J. 3:909-912(1984).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86033734; PubMed=2997153;  
RA Leiter A.B., Montminy M.R., Jamieson E., Goodman R.H.;  
RT "Exons of the human pancreatic polypeptide gene define functional  
domains of the precursor.";  
RL J. Biol. Chem. 260:13013-13017(1985).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85054955; PubMed=6094571;  
RA Leiter A.B., Keutmann H.T., Goodman R.H.;  
RT "Structure of a precursor to human pancreatic polypeptide.";  
RL J. Biol. Chem. 259:14702-14705(1984).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86140715; PubMed=3753985;  
RA Takeuchi T., Gumucio D.L., Yamada T., Meisler M.H., Minth C.D.,  
Dixon J.E., Eddy R.E., Shows T.B.;  
RT "Genes encoding pancreatic polypeptide and neuropeptide Y are on  
human chromosomes 17 and 7";  
RL J. Clin. Invest. 77:1038-1041(1986).  
RN [5]  
RP SEQUENCE OF 69-88.  
RX MEDLINE=84144773; PubMed=6366786;  
RA Schwartz T.W., Hansen H.F., Haakanson R., Sundler F., Tager H.S.;  
RT "Human pancreatic icosapeptide: isolation, sequence, and  
immunocytochemical localization of the COOH-terminal fragment of the  
pancreatic polypeptide precursor";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:708-712(1984).  
CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS  
OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND  
GASTROINTESTINAL FUNCTIONS.  
CC -!- FUNCTION: THE PHYSIOLOGICAL ROLE FOR THE ICOSAPEPTIDE HAS  
NOT YET BEEN ELUCIDATED.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PPY FAMILY.

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CC EMBL; X00491; CAA25161.1; -;  
 CC EMBL; M11726; AAA60156.1; -;  
 CC EMBL; M15788; AAA60161.1; -;  
 CC PIR; A01566; PCBU  
 CC PIR; A22587; A22587.  
 CC HSP; P01302; IBBA.  
 CC Genew; HGNC:9327; PPY.  
 CC MIM; 167780; -;  
 CC InterPro; IPR001955; Pancreatic\_hormn.  
 CC Pfam; PF00159; hormone3; 1.  
 CC PRINTS; PR00278; PANCHORMONE.  
 CC SMART; SM00309; PAH; 1.  
 CC PROSITE; PS00265; PANCREATIC\_HORMONE\_1; 1.  
 CC PROSITE; PS0276; PANCREATIC\_HORMONE\_2; 1.

KW Hormone; Cleavage on pair of basic residues; Pancreas; Signal;  
 KW Amidation.  
 FT SIGNAL 1 29 PANCREATIC\_HORMONE.  
 FT PEPTIDE 30 65 PANCREATIC\_ICOSAPEPTIDE.  
 FT PROPER 69 88  
 FT MOD\_RES 89 95  
 FT MOD\_RES 65 65 AMIDATION (G-66 PROVIDE AMIDE GROUP).  
 FT CONFLICT 86 86 V -> I (IN REF. 4).  
 SQ SEQUENCE 95 AA; 10445 MW; 44F0265092F9C4A0 CRC64;

Query Match 45.8%; Score 441.5; DB 1; Length 95;  
 Best Local Similarity 53.4%; Pred. No. 2e-27;  
 Matches 95; Conservative 0; Mismatches 0; Indels 83; Gaps 1;  
 QY 1 MAAARCLSLLLSTCVALLQLLQAGCAPLEPVYVPGDNATPEQMAQYAADLRRYINML 60  
 Db 1 MAAARCLSLLLSTCVALLQLLQAGCAPLEPVYVPGDNATPEQMAQYAADLRRYINML 60  
 QY 61 TRPRCPVQLGREIPAPGTGLPLHPGHTLSAPAPAPSRPALGKTHLCSTGLDQCALGK 120  
 Db 61 TR-----  
 QY 121 MVPTGRYETGGLAPGHSACPCCLFPYRGRKHEDTLAFSEWGSHPAAVPRELSPLDL 178  
 Db 63 -----PRYGRKHEDTLAFSEWGSHPAAVPRELSPLDL 95

## RESULT 2

ID PAHO\_BOVIN STANDARD; PRT; 131 AA.  
 AC P01302;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pancreatic hormone precursor (pancreatic polypeptide) (PP).  
 GN PPY.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95132646; PubMed=7811336;  
 RA Herzog H., Hort Y., Schneider R., Shine J.;  
 RT "Seminaplasm: recent evolution of another member of the  
 RT neuropeptide Y gene family."  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:594-598(1995).  
 RN [2]  
 RP SEQUENCE OF 30-65.

RA Chance R.E., Johnson M.G., Hoffmann J.A., Jones W.E.,  
 RA Koffenberger J.E. Jr.;  
 RL Unpublished results, cited by:  
 RL Chance R.E., Moon N.E., Johnson M.G.;  
 RL (In) Jaffe B.M., Behrman H.R. (eds.);  
 RL Methods of hormone radioimmunoassay (2nd ed.), pp.657-672,  
 RL Academic Press, New York and London (1979).  
 RN [3]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=92135211; PubMed=1734969;  
 RX Li X., Sutcliffe M.J., Schwartz T.W., Dodson C.M.;  
 RT "Sequence-specific 1H NMR assignments and solution structure of  
 RT bovine pancreatic polypeptide";  
 RL Biochemistry 31:1245-1253(1992)  
 CC -!- FUNCTION: PANCREATIC\_HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS  
 CC OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND  
 CC GASTROINTESTINAL FUNCTIONS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.  
 CC -----  
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CC EMBL; L33970; AAA98526.1; -;  
 CC FIR; A01570; PCBO.  
 CC PDB; 1BBA; 31-OCT-93.  
 CC InterPro; IPR001955; Pancreatic\_hormn.  
 CC Pfam; PF00159; hormone3; 1.  
 CC PRINTS; PR00278; PANCHORMONE.  
 CC SMART; SM00309; PAH; 1.  
 CC PROSITE; PS00265; PANCREATIC\_HORMONE\_1; 1.  
 CC PROSITE; PS0276; PANCREATIC\_HORMONE\_2; 1.  
 KW Hormone; Cleavage on pair of basic residues; Pancreas; Signal;  
 KW Amidation; 3D-structure.  
 FT SIGNAL 1 29  
 FT PEPTIDE 30 65 PANCREATIC\_HORMONE.  
 FT PEPTIDE 69 89 C-TERMINAL PEPTIDE 1 (POTENTIAL).  
 FT PEPTIDE 93 131 C-TERMINAL PEPTIDE 2 (POTENTIAL).  
 FT MOD\_RES 65 65 AMIDATION (G-66 PROVIDE AMIDE GROUP).  
 FT TURN 43 44  
 FT HELIX 45 60  
 SQ SEQUENCE 131 AA; 14375 MW; DCDFF1011C67DF9B CRC64;

Query Match 36.3%; Score 349.5; DB 1; Length 131;  
 Best Local Similarity 48.5%; Pred. No. 2.7e-20;  
 Matches 83; Conservative 3; Mismatches 26; Indels 59; Gaps 2;  
 QY 1 MAAARCLSLLLSTCVALLQLLQAGCAPLEPVYVPGDNATPEQMAQYAADLRRYINML 60  
 Db 1 MAAARCLFLLLSTCVALLQLLQAGCAPLEPVYVPGDNATPEQMAQYAADLRRYINML 60  
 QY 61 TRPRCPVQLGREIPAPGTGLPLHPGHTLSAPAPAPSRPALGKTHLCSTGLDQCALGK 120  
 Db 61 TRPR-----YGK 67

## RESULT 3

PAHO\_CANFA  
 ID PAHO\_CANFA STANDARD; PRT; 93 AA.  
 AC P01299;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pancreatic hormone precursor (pancreatic polypeptide) (PP).



GN PPV  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90331935; PubMed=3079195;  
 RA Toothman P., Paquette T.L.;  
 RT "Canine pancreatic polypeptide complementary deoxyribonucleic acid  
 RT sequence: pancreatic polypeptide and insulin messenger ribonucleic  
 RT acid distribution in the lobes of the pancreas.";  
 RL Mol. Endocrinol. 1:413-419(1987).  
 RN (2)  
 RN SEQUENCE OF 30-65.  
 RP Chance R.E., Johnson M.G., Hoffmann J.A., Jones W.E.,  
 RA Koffenberger J.E. Jr.;  
 RL Unpublished results, cited by:  
 RP Chance R.E., Moon N.E., Johnson M.G.;  
 (In) Jaffe B.M., Behrman H.R. (eds.);  
 Methods of hormone radioimmunoassay (2nd ed.), pp.657-672,  
 Academic Press, New York and London (1979).  
 RN (3)  
 RN SEQUENCE OF 69-88.  
 RX MEDLINE=82080694; PubMed=7031480;  
 RA Schwartz T.W., Tager H.S.;  
 RT "Isolation and biogenesis of a new peptide from pancreatic islets.";  
 RL Nature 294:589-591(1981).  
 RN (4)  
 RN SEQUENCE OF 89-93.  
 RX MEDLINE=87156600; PubMed=3827854;  
 RA Schwartz T.W.;  
 RL Unpublished results, cited by:  
 RL Nielsen H.V., Gether U., Schwartz T.W.;  
 RL Biochem. J. 240:69-74(1986).  
 CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS  
 CC OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND  
 CC GASTROINTESTINAL FUNCTIONS.  
 CC -!- FUNCTION: THE PHYSIOLOGICAL ROLE FOR THE ICOSAPEPTIDE HAS  
 CC NOT YET BEEN ELUCIDATED.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.  
 CC  
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 CC  
 CC EMBL; M35596; AAA30886.1; --  
 CC PIR; A01567; PCDG.  
 CC PIR; A40904; 1BBA.  
 CC HSSP; P01302; 1BBA.  
 CC InterPro; IPR001955; Pancreatic\_hormn.  
 CC Pfam; PF00159; hormone3; 1.  
 CC PRINTS; PR00278; PANCHORMONE.  
 CC SMART; SM00309; PAH; 1.  
 CC PROSITE; PS00265; PANCREATIC\_HORMONE\_1; 1.  
 CC PROSITE; PS50276; PANCREATIC\_HORMONE\_2; 1.  
 CC Hormone; Cleavage on pair of basic residues; Signal;  
 KW Amidation.  
 FT SIGNAL 1 29  
 FT PEPTIDE 30 65 PANCREATIC\_HORMONE.  
 FT PEPTIDE -69 88 PANCREATIC\_ICOSAPEPTIDE.  
 FT PROPEP 89 93  
 FT MOD RES 65 65  
 SQ SEQUENCE 93 AA; 10427 MW; B88DD6D1F0281F413 CRC64;  
 Query Match 31.7%; Score 305.5; DB 1; Length 93;  
 Best Local Similarity 40.5%; Pred. No. 4.3e-17;  
 Matches 70; Conservative 5; Mismatches 15; Indels 83; Gaps 1;

Qy 1 MAARLCISLLSTCVALLQPLLAGQAGAPLEPVPGDNATPEOMAQYAADLRRYINML 60  
 Db 1 MPAAACRCLFLLLSACVALLQPLGTRGAPLEPVPGDDATPEOMAQYAAELRRYINML 60  
 Qy 61 TRPRCVQPGREIPAPGTLPLHIFGHTLSAPAPAPSRPALGKTHGLCTGLDQCALGK 120  
 Db 61 TR----- 62  
 Qy 121 MWPTGRVETOGGLAPGHSACPCCLFPBRYCKRHKEDTLAFSEWGSFHAAPREL 173  
 Db 63 -----PRYKGRDRGEMRDILEWGSFHAAPREL 90  
 RESULT 4  
 PAHO\_MOUSE STANDARD; PRT; 100 AA.  
 AC P10601;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pancreatic hormone precursor (Pancreatic polypeptide) (PP).  
 GN PPY.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88139354; PubMed=3343236;  
 RA Yonekura H., Nata K., Watanabe T., Kuraashina Y., Yamamoto H.,  
 RA Okamoto H.;  
 RT "Mosaic evolution of prepancreatic polypeptide. II. Structural  
 RT conservation and divergence in pancreatic polypeptide gene.";  
 RL J. Biol. Chem. 263:2990-2997(1988).  
 CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS  
 CC OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND  
 CC GASTROINTESTINAL FUNCTIONS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.  
 CC  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL; M18208; AAA39967.1; --  
 CC PIR; B28261; B28261.  
 CC HSSP; P01302; 1BBA.  
 CC MGD; MGI:97753; PPY.  
 CC InterPro; IPR001955; Pancreatic\_hormn.  
 CC Pfam; PF00159; hormone3; 1.  
 CC PRINTS; PR00278; PANCHORMONE.  
 CC SMART; SM00309; PAH; 1.  
 CC PROSITE; PS00265; PANCREATIC\_HORMONE\_1; 1.  
 CC PROSITE; PS50276; PANCREATIC\_HORMONE\_2; 1.  
 CC Hormone; Amidation; pancreas; Cleavage on pair of basic residues;  
 KW Signal.  
 FT SIGNAL 1 29  
 FT PEPTIDE 30 65 PANCREATIC\_HORMONE.  
 FT PEPTIDE 69 100 C-TERMINAL PEPTIDE.  
 FT MOD RES 65 65  
 SQ SEQUENCE 100 AA; 11020 MW; A0D0D04FB7DFB9D9 CRC64;  
 Query Match 27.0%; Score 260.5; DB 1; Length 100;  
 Best Local Similarity 61.1%; Pred. No. 1.2e-13;  
 Matches 58; Conservative 5; Mismatches 25; Indels 7; Gaps 2;  
 Qy 1 MAARLCISLLSTCVALLQPLLAGQAGAPLEPVPGDNATPEOMAQYAADLRRYINML 60  
 Db 1 MPAAACRCLFLLLSACVALLQPLGTRGAPLEPVPGDDATPEOMAQYAAELRRYINML 60

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Db 1 MAVAYCCLSLFLVSTWVALLQPLQCTWGPALBPMYBGDYATPEQMAQYETQLRYINTL 60
QY 61 TRPRVCVPGREIPAGTGLPLHPHIGTSLSPAP 95
Db 61 TRPR----YGRABEENTGG---LPGVQLSPCTSP 88

RESULT 5
PAHO_FELCA
ID PAHO_FELCA STANDARD; PRT; 66 AA.
AC P06984;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pancreatic hormone precursor (Pancreatic polypeptide) (PP) (Fragment).
GN PPY.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Feliidae; Felis.
OX NCBI_TaxID=9685;
[1]
SEQUENCE.
MEDLINE=87156600; PubMed=3827854;
RA Nielsen H.V., Gether U., Schwartz T.W.;
RT "Cat pancreatic eicosapeptide and its biosynthetic intermediate.
RT Conservation of a nonbasic processing site.";
RL Biochem. J. 240:69-74(1986).
CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
CC OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
CC GASTROINTESTINAL FUNCTIONS.
CC -!- FUNCTION: THE PHYSIOLOGICAL ROLE FOR THE ICOSAPEPTIDE HAS
CC NOT YET BEEN ELUCIDATED.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: GLY-LYS-ARG AT POSITIONS 37 TO 39 WERE INCLUDED BY
CC HOMOLOGY WITH OTHER PANCREATIC HORMONE TYPE PRECURSOR SEQUENCE.
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
DR PIR; A26073; PCCT.
DR HSGP; P01302; 1BBA.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormones; 1.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS0276; PANCREATIC_HORMONE_2; 1.
KW Hormone; Amidation; Pancreas; Cleavage on pair of basic residues.
FT NON_TER 1
FT PEPTIDE 1 36 PANCREATIC HORMONE.
FT MOD_RES 40 59 PANCREATIC ICOSAPEPTIDE.
FT MOD_RES 36 36 AMIDATION (G-37 PROVIDE AMIDE GROUP).
FT NON_TER 66
FT SEQUENCE 66 AA; 7483 MW; 2D3A94BD9063A83D CRC64;

Query Match 25.98; Score 249.5; DB 1; Length 66;
Best Local Similarity 36.94; Pred. No. 5.6e-13;
Matches 55; Conservative 5; Mismatches 6; Indels 83; Gaps 1;

QY 30 APLEPVYFGDNATPEQMAQYAADLRRYINMLTRPRVCVPGLGREIPAGTGLHPHIGTSL 89
Db 1 APLEPVYFGDNATPEQMAQYAAELRRYINMLTR----- 33
QY 90 SPAPAPSRPALGKTGHLCSGLDQCALGMVPTGTYETGGLAPGHSACPCLPPRYG 149
Db 34 -----PRYG 37

QY 150 KHKEDTLAFSEWGSPPHAAPRELSPDL 178
Db 38 KDRGETLDILEWGSPPHAAPRELSPMDV 66

RESULT 6
PAHO_CAVPO
ID PAHO_CAVPO STANDARD; PRT; 126 AA.
AC P13083;
DT 01-JAN-1990 (Rel. 13, Created)

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DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pancreatic hormone precursor (Pancreatic polypeptide) (PP).
GN PPY.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=88139344; PubMed=2830269;
RA Blackstone C.D., Seino S., Takeuchi T., Yamada T., Steiner D.F.;
RT "Novel organization and processing of the guinea pig pancreatic
RT polypeptide precursor.";
RL J. Biol. Chem. 263:2911-2916(1988).
CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
CC OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
CC GASTROINTESTINAL FUNCTIONS.
CC -!- FUNCTION: THE PHYSIOLOGICAL ROLE FOR THE ICOSAPEPTIDE HAS
CC NOT YET BEEN ELUCIDATED.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
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CC
CC EMBL; M29543; AAA37051.1;
DR PIR; A28256; A28256.
DR HSGP; P01302; 1BBA.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormones; 1.
DR PRINTS; PR00278; PANCHORMONE.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS0276; PANCREATIC_HORMONE_2; 1.
KW Hormone; Cleavage on pair of basic residues; Pancreas; Signal;
KW Amidation.
FT SIGNAL 1 26 PANCREATIC HORMONE.
FT PEPTIDE 27 62 PANCREATIC ICOSAPEPTIDE.
FT PEPTIDE 67 126 AMIDATION (G-63 PROVIDE AMIDE GROUP).
FT MOD_RES 62 62
FT SEQUENCE 126 AA; 13488 MW; 76C131560F566326 CRC64;

Query Match 25.44; Score 244.5; DB 1; Length 126;
Best Local Similarity 52.74; Pred. No. 2.4e-12;
Matches 59; Conservative 9; Mismatches 29; Indels 15; Gaps 4;

QY 1 MAARCLSLLLSTCVALLQPLLGAGAPLEVPYFGDNATPEQMAQYAADLRRYINML 60
Db 1 MTATRCCLWLLLTGTCMALLPE---AWGAPLEVPYFGDTPQMAQYAAELRRYINML 57
QY 61 TRPRVCVPGLGREIPAGTGLHPHIGTSLSPA-----PAPAPSRPALGKTG 106
Db 58 TRPR----YGKSAEDALGLPWRQSHAAAPGSHRHPAGLPA--AKGCTG 103

RESULT 7
PAHO_RAT
ID PAHO_RAT STANDARD; PRT; 98 AA.
AC P06303;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatic hormone precursor (Pancreatic polypeptide) (PP).
GN PPY.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

```

OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86196026; PubMed=3009446;  
 RA Yamamoto H., Nata K., Okamoto H.;  
 RL "Mosaic evolution of prepropancreatic polypeptide.";  
 RT J. Biol. Chem. 261:6156-6159(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88139354; PubMed=3343236;  
 RA Yonekura H., Nata K., Watanabe T., Kurashina Y., Yamamoto H.,  
 RL Okamoto H.;  
 RT "Mosaic evolution of prepropancreatic polypeptide. II. Structural  
 conservation and divergence in pancreatic polypeptide gene.";  
 RL J. Biol. Chem. 263:2990-2997(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89104395; PubMed=3214179;  
 RA Kopin A.S., Toder A.E., Leiter A.B.;  
 RT "Different splice site utilization generates diversity between the  
 rat and human pancreatic polypeptide precursors.";  
 Arch. Biochem. Biophys. 267:742-748(1988).  
 CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS  
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND  
 GASTROINTESTINAL FUNCTIONS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DOMAIN: IN RAT PRECURSOR, THE PEPTIDE WHICH IS FOUND AT THE C-  
 TERMINAL OF PANCREATIC HORMONE DOES NOT SHOW ANY HOMOLOGY TO  
 PANCREATIC ISOCAPTEIDE WHICH IS FOUND AT THE C-TERMINAL OF THE  
 PRECURSOR OF HUMAN PANCREATIC HORMONE.  
 CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.  
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 CC  
 DR EMBL; M13588; AAA41923.1; -;  
 DR EMBL; M18207; AAA41922.1; -;  
 DR EMBL; M27450; AAA99236.1; -;  
 DR PIR; A01571; PCRT.  
 DR PIR; A28261; A28261.  
 DR PIR; S06472; S06472.  
 DR HSSP; P01302; IBEA.  
 DR InterPro; IPR001955; Pancreatic\_hormn.  
 DR PRINTS; PR00278; PANCHORMONE.  
 DR SMART; SM00309; PAH; 1.  
 DR PROSITE; PS00265; PANCREATIC\_HORMONE\_1; 1.  
 DR PROSITE; PS0276; PANCREATIC\_HORMONE\_2; 1.  
 DR Hormone; Amidation; Pancreas; Cleavage on pair of basic residues;  
 KW Signal.  
 FT SIGNAL 1 29  
 FT PEPTIDE 30 65 PANCREATIC HORMONE.  
 FT PEPTIDE 69 98 C-TERMINAL PEPTIDE.  
 FT MOD RES 65 65 AMIDATION (G-66 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 98 AA; 10975 MW; 56AC03356D248FB0 CRC64;  
 Query Match 24.5%; Score 236.5; DB 1; Length 98;  
 Best Local Similarity 49.6%; Pred. No. 7.8e-12;  
 Matches 61; Conservative 6; Mismatches 27; Indels 29; Gaps 5;  
 QY 1 MAAARCLSLLLSTCVALLQPLGAGAPLPVPGDNATPEQMAQAAADLRYYNNL 60  
 DB 1 MAVAYCISLFLSTWALLQPLQAGAPLPVPGDYATHEQRAQVETQLRYINTL 60  
 QY 61 TRPRCVPGREIPAGTGLPHHTPGHTLSPAPAPSRPALGKTGHLGST---GLDQCA 117  
 DB 61 TRPR---YGRK---DEDTAG---LPGRLPP-----CTSLVLGLMPCA 94

QY 118 LCK 120  
 DB 95 AAR 97  
 RESULT 8  
 PAHO SHEEP  
 ID PAHO SHEEP STANDARD; PRT; 59 AA.  
 AC P01301;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pancreatic hormone precursor (Pancreatic polypeptide) (PP) (Fragment).  
 GN PPY.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE OF 1-36.  
 RA Chance R.E., Johnson M.G., Hoffmann J.A., Jones W.E.,  
 RA Koffenberger J.E. Jr.;  
 RL Unpublished results, cited by:  
 RL Chance R.E., Moon N.E., Johnson M.G.;  
 RL (in) Jaffe B.M., Behrman H.R. (eds.);  
 RL Methods of hormone radioimmunoassay (2nd ed.), pp. 657-672,  
 RL Academic Press, New York and London (1979).  
 RN [2]  
 RP SEQUENCE OF 40-59.  
 RX MEDLINE=84208777; PubMed=6723953;  
 RA Schwartz T.W., Hansen H.F.;  
 RT "Isolation of ovine pancreatic icosa-peptide: a peptide product  
 containing one cysteine residue.";  
 RL FEBS Lett. 168:293-298(1984).  
 CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS  
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND  
 GASTROINTESTINAL FUNCTIONS.  
 CC -!- FUNCTION: THE PHYSIOLOGICAL ROLE FOR THE ICOSAPEPTIDE HAS  
 NOT YET BEEN ELUCIDATED.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MISCELLANEOUS: GLY-LYS-ARG AT POSITIONS 37 TO 39 WERE INCLUDED BY  
 HOMOLOGY WITH OTHER PANCREATIC HORMONE TYPE PRECURSOR SEQUENCE.  
 CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.  
 DR PIR; A01569; PCSH.  
 DR HSSP; P01302; IBEA.  
 DR InterPro; IPR001955; Pancreatic\_hormn.  
 DR Pfam; PF00159; hormone3; 1.  
 DR ProDom; PD001267; Pancreatic\_hormn; 1.  
 DR SMART; SM00309; PAH; 1.  
 DR PROSITE; PS00265; PANCREATIC\_HORMONE\_1; 1.  
 DR PROSITE; PS0276; PANCREATIC\_HORMONE\_2; 1.  
 DR Hormone; Cleavage on pair of basic residues; Amidation; Pancreas.  
 KW NON\_TER 1 1  
 FT PEPTIDE 1 36 PANCREATIC HORMONE.  
 FT PEPTIDE 40 59 PANCREATIC ICOSAPEPTIDE.  
 FT MOD RES 36 36 AMIDATION (G-37 PROVIDE AMIDE GROUP).  
 FT NON\_TER 59 59  
 SQ SEQUENCE 59 AA; 6698 MW; 4DD271D6091A3D57 CRC64;  
 Query Match 21.5%; Score 207.5; DB 1; Length 59;  
 Best Local Similarity 35.2%; Pred. No. 7.8e-10;  
 Matches 50; Conservative 2; Mismatches 7; Indels 83; Gaps 1;  
 QY 30 APLEPVPGDNATPEQMAQAAADLRYYNNLTPRCVPGDLPGLHPGHTL 89  
 DB 1 ASLEPYPGDNATPEQMAQAAADLRYYNNLTPR----- 33  
 QY 90 SPAPAPSRPALGKTGHLCTGLDQCAKGMVGTGTLGAPGHACPCCLFPBRYG 149  
 DB 34 ----- 37  
 QY 150 KRHKEDTLAFSEWGSPPHAAVPR 171



PAHO\_2QUZE  
ID PAHO\_EQUZE STANDARD; PRT; 36 AA.  
AC P38000;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pancreatic hormone (Pancreatic polypeptide) (PP).  
GN PPY.  
OS Equus zebra (Mountain zebra), and  
OS Equus caballus przewalskii (Przewalski's horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCB1\_TaxID=9791, 9798;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pancreas;  
RX MEDLINE=92225314; PubMed=1808025;  
RA Henry J.S., Lance V.A., Conlon J.M.;  
RT "Primary structure of pancreatic polypeptide from four species of  
Perissodactyla (Przewalski's horse, zebra, rhino, tapir).";  
Gen. Comp. Endocrinol. 84:440-446(1991).  
CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS  
OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND  
GASTROINTESTINAL FUNCTIONS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.  
DR PIR: A61132; A61132.  
DR PIR: D61132; D61132.  
DR HSSP; P01302; 1BBA.  
DR InterPro; IPR001955; Pancreatic\_horm.  
DR Pfam; PF00159; hormone3; 1.  
DR PRINTS; PR00278; PANCHORMONE.  
DR SMART; SM00309; PAH; 1.  
DR PROSITE; PS00265; PANCREATIC\_HORMONE\_1; 1.  
DR PROSITE; PS0276; PANCREATIC\_HORMONE\_2; 1.  
KW Hormone; Amidation; Pancreas.  
FT MOD\_RES 36  
SQ SEQUENCE 36 AA; 4215 MW; 761ADA6CC1A6308F CRC64;  
Query Match 18.7%; Score 180; DB 1; Length 36;  
Best Local Similarity 94.3%; Pred. No. 6.1e-08;  
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64  
DB 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35  
RESULT 13  
PAHO\_PIG  
ID PAHO\_PIG STANDARD; PRT; 36 AA.  
AC P01300;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pancreatic hormone (Pancreatic polypeptide) (PP).  
GN PPY.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCB1\_TaxID=9823;  
RN [1]  
RP SEQUENCE.  
RC Chance R.E., Johnson M.G., Hoffmann J.A., Lin T.-M.;  
RA (In) Baba S., Kaneko T., Yanaihara N. (eds.);  
RL proinsulin, insulin, c-peptide, pp.419-425, Excerpta Medica,  
RL Amsterdam (1979).  
CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS  
OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND  
GASTROINTESTINAL FUNCTIONS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.  
DR PIR: A01568; PCPG.

HSSP; P01302; 1BBA.  
DR InterPro; IPR001955; Pancreatic\_horm.  
DR Pfam; PF00159; hormone3; 1.  
DR PRINTS; PR00278; PANCHORMONE.  
DR SMART; SM00309; PAH; 1.  
DR PROSITE; PS00265; PANCREATIC\_HORMONE\_1; 1.  
DR PROSITE; PS0276; PANCREATIC\_HORMONE\_2; 1.  
KW Hormone; Amidation; Pancreas.  
FT MOD\_RES 36  
SQ SEQUENCE 36 AA; 4198 MW; 7611DD1DC71A6308F CRC64;  
Query Match 18.4%; Score 177; DB 1; Length 36;  
Best Local Similarity 94.3%; Pred. No. 1e-07;  
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64  
DB 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35  
RESULT 14  
PAHO\_CERSI  
ID PAHO\_CERSI STANDARD; PRT; 36 AA.  
AC P37959;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pancreatic hormone (Pancreatic polypeptide) (PP).  
GN PPY.  
OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.  
OX NCB1\_TaxID=9807;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pancreas;  
RX MEDLINE=92225314; PubMed=1808025;  
RA Henry J.S., Lance V.A., Conlon J.M.;  
RT "Primary structure of pancreatic polypeptide from four species of  
Perissodactyla (Przewalski's horse, zebra, rhino, tapir).";  
Gen. Comp. Endocrinol. 84:440-446(1991).  
CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS  
OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND  
GASTROINTESTINAL FUNCTIONS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.  
DR PIR: B61132; B61132.  
DR HSSP; P01302; 1BBA.  
DR InterPro; IPR001955; Pancreatic\_horm.  
DR Pfam; PF00159; hormone3; 1.  
DR PRINTS; PR00278; PANCHORMONE.  
DR SMART; SM00309; PAH; 1.  
DR PROSITE; PS00265; PANCREATIC\_HORMONE\_1; 1.  
DR PROSITE; PS0276; PANCREATIC\_HORMONE\_2; 1.  
KW Hormone; Amidation; Pancreas.  
FT MOD\_RES 36  
SQ SEQUENCE 36 AA; 4214 MW; 761B716F8CE2908F CRC64;  
Query Match 18.3%; Score 176; DB 1; Length 36;  
Best Local Similarity 91.4%; Pred. No. 1.2e-07;  
Matches 32; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
OY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64  
DB 1 SPLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35  
RESULT 15  
PAHO\_ERIEU  
ID PAHO\_ERIEU STANDARD; PRT; 36 AA.  
AC P41335;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pancreatic hormone (Pancreatic polypeptide) (PP).  
 GN PPY.  
 OS Erinaceus europaeus (Western European hedgehog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.  
 OC NCBI\_TaxID=9365;  
 RN (1)  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=94052825; PubMed=8234904; Thim L.;  
 RA Marks N.J., Shaw C., Halton D.W., Thim L.;  
 RT "The primary structure of pancreatic polypeptide from a primitive  
 insectivorous mammal, the European hedgehog (Erinaceus europaeus).";  
 RL Regul. Pept. 47:179-185(1993).  
 CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS  
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND  
 GASTROINTESTINAL FUNCTIONS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.  
 HSP; P01302; IBBA.  
 InterPro; IPR001955; Pancreatic\_horm.  
 Pfam; PF00159; hormone3; 1.  
 DR PRINTS; PR00278; PANCHORMONE.  
 DR SMART; SM00309; PAH; 1.  
 DR PROSITE; PS00265; PANCREATIC\_HORMONE\_1; 1.  
 DR PROSITE; PS0276; PANCREATIC\_HORMONE\_2; 1.  
 KW Hormone; Amidation; Pancreas.  
 FT MOD RES 36 36 AMIDATION.  
 SQ SEQUENCE 36 AA; 4234 MW; 7609C6989148208F CRC64;

Query Match 17.9%; Score 173; DB 1; Length 36;

Best Local Similarity 94.1%; Pred. No. 2.1e-07;

Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 31 PLEVPYGDNATPEQMAQYAADLRRYINMLTRPR 64

Db 2 PLEVPYGDNATPEQMAHYAAELRRYINMLTRPR 35

Search completed: March 1, 2003, 09:11:58

Job time : 13 secs